REMARKS

Claims 1-3, 8, 10, and 11 have been amended. Claims 9, 12-43, and 45-54 have been canceled without prejudice or disclaimer. Claims 1-8, 10, 11, and 44 are pending in the instant application. Support for the amendments to the claims can be found in the specification at, for example, page 10, line 9; page 14, line 16; page 17, line 1; in Figures 1A-1B, and in the Sequence Listing. No new matter has been added as a result of the above-described amendments. The rejections set forth in the Office Action have been overcome by amendment or are traversed by argument below.

1. Claim of priority

The Office Action asserts that because the nucleotide sequence of SEQ ID NO: 1, the DNA insert in ATCC Deposit No. PTA-1882, and the limitation "at least about 70 percent identical to the polypeptide as set forth in SEQ ID NO: 2" are not disclosed in U.S. Provisional Application No. 60/188,786 (the '786 application), from which the instant application claims priority, in the manner provided by 35 U.S.C. § 112, first paragraph, these limitations are not entitled to the benefit of the filing date of the '786 application under 35 U.S.C. § 119(e). The Action states that the subject matter recited in claims 1, 2, 4-8, 10, 11, and 44 is therefore entitled only to the March 13, 2001 filing date of instant application. Applicants respectfully contend that only the initial priority determination (*i.e.*, that the nucleotide sequence of SEQ ID NO: 1 is not entitled to the benefit of the March 13, 2000 filing date of the '786 application) is relevant to the rejections made in the instant Action (*see* discussion in sections 3 and 5 below), and therefore, that only this determination must be addressed.

As shown in Exhibit A, the nucleotide sequence disclosed in Figure 1 of the '786 application is 100% identical to nucleotide residues 610 through 1242 of the nucleotide sequence set forth in SEQ ID NO: 1. However, because the FGF-L open reading frame also comprises nucleotide residues 610 through 1242 of the nucleotide sequence set forth in SEQ ID NO: 1, residues 1 through 609 merely constitute the 5' untranslated portion of the FGF-L cDNA sequence and residues 1246 through 1330 merely constitute the 3' untranslated portion of the FGF-L cDNA sequence (residues 1243 through 1245 constituting the stop codon). Applicants respectfully contend that the portion of the nucleotide sequence of SEQ ID NO: 1 that encodes FGF-L polypeptide (*i.e.*, the amino acid

McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
Chicago, Illinois 60606
(312) 913-0001

sequence set forth in SEQ ID NO: 2) is disclosed in U.S. Provisional Application No. 60/188,786 (the '786 application) in the manner provided by 35 U.S.C. § 112, first paragraph, and therefore, that this sequence is entitled to the benefit of the filing date of the '786 application under 35 U.S.C. § 119(e).

2. Rejection of claims 1-8, 10, 11, and 44 under 35 U.S.C. § 101

The Office Action asserts a rejection of claims 1-8, 10, 11, and 44 under 35 U.S.C. § 101. The Action states that the claimed invention is not supported by either a specific and substantial asserted utility or a well-established utility. The Action also states that, in view of Galzie *et al.*, 1997, *Biochem. Cell Biol.* 75:669-85, which discloses that the FGF family of proteins encompasses a group of polypeptide mitogens eliciting a wide variety of responses, and Koga *et al.*, 1999, *Biochem. Biophys. Res. Commun.* 261:756-65, which discloses that the expression pattern of FGF-20 and FGF-9 differs, the members of the FGF family of proteins lack a common utility applicable to all members of this family. The Action further states that one of ordinary in the art would not accept mere homology as establishing a function of a protein. Applicants traverse this rejection.

Applicants contend that the specification contains an assertion of a specific and substantial utility for the claimed invention that would be credible to one of ordinary skill in the art. The instant specification teaches a human cDNA of 1330 nucleotides encoding an FGF-L polypeptide of 211 amino acids (Figures 1A-1B). The instant application also teaches that FGF-L polypeptides share a high degree of sequence similarity with the members of the FGF family of proteins, and the highest degree of sequence identity with FGF-9 and FGF-16 (Figures 2-4 and page 74, lines 18-19). A ClustalW sequence alignment of the amino acid sequences of FGF-9 or FGF-16 and human FGF-L polypeptide clearly illustrates the close structural relationship between FGF-L polypeptide and FGF-9 and FGF-16 (*see* Exhibit B); the former sequence sharing 68% sequence identity (and 80% similarity) with FGF-L polypeptide and the latter sequence sharing 62% sequence identity (and 82% similarity) with FGF-L polypeptide. This close relationship is further illustrated in the guide tree shown in Exhibit C (the sequence alignment and guide tree shown in Exhibits B and C were prepared using the application MacVector 7.1.1; Accelrys; Cambridge, UK, at the default settings and amino acid sequences that were publicly available at the time the instant application was filed). In addition, nearly all of the related amino acid sequences identified in a BLAST search using the human FGF-L

McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
Chicago, Illinois 60606
(312) 913-0001

amino acid sequence (SEQ ID NO: 2) are members of the FGF family of proteins (*see* Exhibit D; sequences that were publicly available at the time the instant application was filed are indicated in bold). Applicants contend that such sequence analyses could be performed at the time the instant application was filed using the teachings in the instant application and knowledge in the art by one having but ordinary skill in the art.

Applicants also note that the human FGF-L polypeptide disclosed in the instant application shares substantial amino acid sequence similarity with the *Xenopus* FGF molecule, XFGF-20, disclosed by Koga *et al.*, 1999, *Biochem. Biophys. Res. Commun.* 261:756-65 (*see* Exhibit E, which was prepared using the application MacVector 7.1.1 at the default settings). Koga *et al.* disclose that XFGF-20 is expressed in *Xenopus* embryos during the blastula stage and in the stomachs and testis of adults. Applicants contend that one of ordinary skill in the art, at the time the application was filed, would have recognized that the human FGF-L polypeptide disclosed in the instant application, which shares 80% sequence identity and 89% sequence similarity with human FGF-L polypeptide, is, in fact, the human ortholog of XFGF-20.

Applicants contend that based on the totality of the evidence of record, one of ordinary skill in the art would recognize that FGF-L: polypeptide is a member of the FGF family of proteins – namely, FGF-20. In fact, the results of the BLAST search described above indicate that those of ordinary skill in the art, absent Applicants' teaching, *have* recognized that the human polypeptide set forth in SEQ ID NO: 2 *is* a member of the FGF family of proteins (*i.e.*, FGF-20), albeit subsequent to Applicants' identification of this member of the FGF family (*see* Kirikoshi *et al.*, GenBank Accession Nos. BAB03633, published August 2, 2000, JC7353, published December 1, 2000, and Q9NP95, published October 16, 2001; Omachi *et al.*, GenBank Accession No. BAB03530, published November 11, 2000; and Jeffers *et al.*, GenBank Accession No. NP_062825, published April 6, 2003). Moreover, as members of the FGF family have substantial real world use, for example, as regulators of cell proliferation, differentiation, and function (Galzie *et al.*, 1997, *Biochem. Cell Biol.* 75:669-85), and the teachings of Koga *et al.* indicate that FGF-20 plays a role in cell differentiation at the blastula stage of development,, Applicants contend that one or ordinary skill in the art would recognize that the claimed molecules have credible, specific, and substantial utility.

Applicants contend that because the instant application contains an assertion of a specific and

McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
Chicago, Illinois 60606
(312) 913-0001

substantial utility for the claimed invention credible to one of ordinary skill in the art, the rejection under 35 U.S.C. § 101 should be withdrawn.

3. Rejections of claims 1-8, 10, 11, and 44 under 35 U.S.C. § 112, first paragraph

The Office Action asserts a rejection of claims 1-8, 10, 11, and 44 under 35 U.S.C. § 112, first paragraph, as containing subject matter that was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most clearly connected, to make and use the invention. The Action states that because the claimed invention is not supported by a specific and substantial asserted utility or a well-established utility, one skilled in the art would not know how to use the claimed invention.

Applicants have set forth above affirmative evidence that the asserted utility would be credible to one of ordinary skill in the art. Applicants contend that because the instant application contains an assertion of a specific and substantial utility for the claimed invention that one of ordinary skill in the art would find to be credible, this rejection should be withdrawn.

The Office Action also asserts a rejection of claims 1-8, 10, 11, and 44 under 35 U.S.C. § 112, first paragraph, as containing subject matter that was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most clearly connected, to make and use the invention. The Action states that because ATCC Deposit No. PTA-1882 does not appear to be publicly available or capable of being reproducibly isolated from nature without undue experimentation, and the claims require the use of this deposit, the mere reference to the deposit in the specification is insufficient to ensure that all of the conditions of 37 C.F.R. §§ 1.803-1.809 have been met. The Action also states that a deposit made in full compliance with 37 C.F.R. §§ 1.803-1.809 would satisfy the requirements of 35 U.S.C. § 112, first paragraph, provided that Applicants submit an affidavit or declaration by Applicants or someone associated with the patent owner who is in a position to make such assurances, or a statement by an attorney of record over his or her signature, stating that a deposit has been made under the terms of the Budapest Treaty and that all restrictions imposed by the depositor on the availability to the public of the deposited material will be irrevocably removed upon the granting of a patent. The Action further states that the instant specification must be amended to recite the date of the deposit and the complete name and address of the depository, and that the claims must be amended to recite the accession number.

McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
Chicago, Illinois 60606
(312) 913-0001

Pursuant to the Examiner's request, Applicants' representative submits that Applicants deposited cDNA encoding human FGF-L polypeptide with the American Type Culture Collection (ATCC), 10801 University Boulevard, Manassas, VA 20110-2209. The deposit was accepted by the ATCC, an International Depository Authority, under the provisions of the Budapest Treaty, and the deposit was designated as PTA-1882. A copy of the ATCC receipt for this deposit, showing the patent deposit designation (Accession No. PTA-1882) and the date on which the deposit was received by the ATCC (May 17, 2000) is attached. Pursuant to 37 C.F.R. § 1.808(a)(2), the deposit was made under conditions that assure that all restrictions imposed by the depositors on the availability to the public of the deposited material would be irrevocably removed upon the granting of a patent relying on the deposited biological material. In making the deposit, Applicants acknowledged their responsibility, pursuant to 37 C.F.R. § 1.805, to provide a replacement or supplemental deposit if the depository possessing the deposit is unable to furnish samples thereof or is able to furnish samples thereof but the deposit has become contaminated or has lost its capability to function as described in the specification. With regard to the assertion that the date of the deposit and the complete name and address of the depository is not referred to in the body of the specification, Applicants respectfully direct the Examiner's attention to 77, lines 24-27 of the specification where Applicants disclose that a deposit of cDNA encoding human FGF-L polypeptide, subcloned into pGEM-T: JH3 (Promega; Madison, WI), and having Accession No. PTA-1882, was made with the American Type Culture Collection, 10801 University Boulevard, Manassas, VA 20110-2209, on May 17, 2000. With regard to the assertion that the accession number of the deposit is not referred to in the claims, Applicants respectfully direct the Examiner's attention to claims 1(b) and 2(b)-2(d), as originally filed. Applicants contend that all the requirements of 37 C.F.R. §§ 1.801-1.809 have been met. *In re Lundak,* 225 U.S.P.Q. 90 (Fed. Cir. 1985). Withdrawal of this rejection is therefore respectfully solicited.

The Office Action also asserts a rejection of claims 1-8, 10, 11, and 44 under 35 U.S.C. § 112, first paragraph, as containing subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention. The Action states that because the claims do not place any limit on the number of nucleotide substitutions, deletions, insertions, or additions that may be made to the FGF-L molecules of the invention, the claimed genus of nucleic

McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
Chicago, Illinois 60606
(312) 913-0001

acid molecules is highly variant. The Action also states that because one of ordinary skill in the art cannot envision the detailed structure of the genus of nucleic acid molecules encompassed by the claims, and the specification does not contain a sufficient recitation of distinguishing identifying characteristics of the genus, the specification does not meet the written description requirement for claiming such a genus.

Applicants have amended claim 1 to recite an isolated nucleic acid molecule comprising a nucleotide sequence as set forth in SEQ ID NO: 1; a nucleotide sequence comprising nucleotide residues 610 through 1242 of the nucleotide sequence set forth in SEQ ID NO: 1; a nucleotide sequence of the DNA insert in ATCC Deposit No. PTA-1882; a nucleotide sequence encoding the polypeptide as set forth in SEQ ID NO: 2; a nucleotide sequence that hybridizes under at least moderately stringent conditions to the complement of a nucleotide sequence comprising nucleotide residues 610 through 1242 of the nucleotide sequence set forth in SEQ ID NO: 1 or a nucleotide sequence encoding the polypeptide as set forth in SEQ ID NO: 2; or a nucleotide sequence that is complementary to any of these nucleotide sequences. Applicants contend that the genus of molecules encompassed by amended claim 1 is not highly variant, as this claim does not encompass FGF-L molecules containing any number of nucleotide substitutions, and that one of ordinary skill in the art could readily determine the structure of the nucleic acid molecules falling within the scope of this claim. Applicants, therefore, submit that amended claim 1 satisfies the requirements of 35 U.S.C. § 112, first paragraph, and respectfully request that the rejection of this claim on § 112, first paragraph, grounds be withdrawn.

Applicants have amended claim 2 to recite an isolated nucleic acid molecule comprising a region of the nucleotide sequence of SEQ ID NO: 1 or the DNA insert in ATCC Deposit No. PTA-1882 encoding a polypeptide fragment of SEQ ID NO: 2 of at least 50 amino acid residues; a nucleotide sequence that hybridizes under at least moderately stringent conditions to the complement of this nucleotide sequence; or a nucleotide sequence that is complementary to this nucleotide sequence. Applicants note that claim 2, as amended, no longer recites an isolated nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide that is at least 70 percent identical to the polypeptide of SEQ ID NO: 2; a nucleotide sequence encoding an allelic or splice variant of the nucleotide sequence of SEQ ID NO: 1, the nucleotide sequence of the DNA insert in ATCC Deposit No. PTA-1882, or of a nucleotide sequence recited in claim 2; or a region of the

McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
Chicago, Illinois 60606
(312) 913-0001

nucleotide sequence of SEQ ID NO: 1, the DNA insert in ATCC Deposit No. PTA-1882, or a nucleotide sequence recited in claim 2 comprising a fragment of at least about 16 nucleotides. Applicants contend that the genus of molecules encompassed by amended claim 2 is not highly variant, as this claim does not encompass FGF-L molecules containing any number of nucleotide substitutions. Applicants also contend that because amended claim 2 recites only fragments of the disclosed human FGF-L nucleic acid molecule that encode an FGF-L polypeptide fragment of at least 50 amino acid residues, one of ordinary skill in the art could readily determine the structure of nucleic acid molecules falling within the scope of this claim. Applicants, therefore, submit that amended claim 2 satisfies the requirements of 35 U.S.C. § 112, first paragraph, and respectfully request that the rejection of this claim on § 112, first paragraph, grounds be withdrawn.

Applicants have amended claim 3 to recite an isolated nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 with at least one conservative amino acid substitution, wherein the encoded polypeptide is at least 85 percent identical to the polypeptide set forth in SEQ ID NO: 2; a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 having a C- and/or N- terminal truncation, wherein the encoded polypeptide comprises at least 50 amino acid residues; a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 with at least one modification that is a conservative amino acid substitution, C-terminal truncation, or N-terminal truncation, wherein the encoded polypeptide is at least 85 percent identical to the polypeptide set forth in SEQ ID NO: 2 and comprises at least 50 amino acid residues; or a nucleotide sequence that is complementary to any of these nucleotide sequences. Applicants note that claim 3, as amended, no longer recites an isolated nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 with at least one amino acid insertion; a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 with at least one amino acid deletion; a fragment of a nucleotide sequence recited in claim 3 comprising at least 16 nucleotides; or a nucleotide sequence which hybridizes under at least moderately stringent conditions to the complement of a nucleotide sequence recited in claim 3. Applicants also note that the instant application teaches the nucleotide and amino acid sequences for human FGF-L polypeptide (Figures 1A-1B); that FGF-L shares a high degree of amino sequence identity with several other members of the FGF family of proteins (Figures 2-4 and page 74, lines 18-19); that regions in FGF-L polypeptide that are tolerable to conservative amino acid substitution can be

McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
Chicago, Illinois 60606
(312) 913-0001

identified by performing sequence comparisons between FGF-L polypeptide and other related polypeptides (page 20, lines 5-9); and rubrics recognized in the art for making conservative amino acid substitutions (Table I; pages 19-20). Applicants contend, for example, that one of ordinary skill in the art could perform a sequence comparison of the human FGF-L polypeptide disclosed in the instant specification and the FGF-L ortholog disclosed by Koga *et al.* in order to determine the positions within the human FGF-L polypeptide sequence where substitutions, either conservative or nonconservative, would be tolerated, and that such a comparison would be well within the skill of one having ordinary skill in the art. In view of the teachings in the instant application and knowledge in the art at the time the instant application was filed, Applicants contend that one of ordinary skill in the art would understand the scope of species comprising the genus of FGF-L variants defined by claim 3, and that the inventors were in possession of the invention having said scope at the time the application was filed. Applicants, therefore, submit that amended claim 3 satisfies the requirements of 35 U.S.C. § 112, first paragraph, and respectfully request that the rejection of this claim on § 112, first paragraph, grounds be withdrawn.

The Office Action also asserts a rejection of claims 1-8, 10, 11, and 44 under 35 U.S.C. § 112, first paragraph, as containing subject matter that was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most clearly connected, to make and use the invention. The Action states that because the specification lacks sufficient guidance regarding the positions of FGF-L polypeptide that are essential for its biological activity, one of ordinary skill in the art would be left to extensive trial and error experimentation in order to identify polypeptides that retain FGF-L polypeptide function, and therefore, it would require undue experimentation to make and use nucleic acid molecules encoding such polypeptides.

As described above, Applicants have amended claims 1-3 so that they no longer recite an isolated nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide that is at least 70 percent identical to the polypeptide of SEQ ID NO: 2; a nucleotide sequence encoding an allelic or splice variant of the nucleotide sequence of SEQ ID NO: 1, the nucleotide sequence of the DNA insert in ATCC Deposit No. PTA-1882, or of a nucleotide sequence recited in claim 2; a region of the nucleotide sequence of SEQ ID NO: 1, the DNA insert in ATCC Deposit No. PTA-1882, a nucleotide sequence recited in claim 2 comprising a fragment of at least about 16 nucleotides; a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 with at least one amino

McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
Chicago, Illinois 60606
(312) 913-0001

acid insertion; a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 with at least one amino acid deletion; a fragment of a nucleotide sequence recited in claim 3 comprising at least 16 nucleotides; or a nucleotide sequence which hybridizes under at least moderately stringent conditions to the complement of a nucleotide sequence recited in claim 3. Applicants, therefore, contend that the claims, as amended, are not overly broad. Applicants also contend that, in view of the specification's teachings and knowledge in the art, it would not require undue experimentation for one of ordinary skill in the art to make and use the claimed invention, and therefore, Applicants respectfully request that this ground of rejection be withdrawn.

Applicants respectfully contend that rejections based on 35 U.S.C. § 112, first paragraph, have been overcome by amendment or traversed by argument, and request that the Examiner withdraw all rejections made on this basis.

4. Rejections of claims 1-8, 10, 11, and 44 under 35 U.S.C. § 112, second paragraph

The Office Action asserts a rejection of claims 1-8, 10, 11, and 44 under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter that Applicants regard as the invention.

The Action first asserts that claims 8 and 10 are indefinite for reciting the phrase "moderately or highly stringent conditions," because the specification fails to precisely define "moderately or highly stringent conditions." Applicants note that the specification defines the meaning of the terms "moderately stringent conditions" (page 16, lines 3-9) and "highly stringent conditions" (page 15, lines 1-8), and provides examples of each. However, in order to expedite prosecution of the pending claims to allowance, and in Applicants' view because it will have no substantive effect in the proper scope of the pending claims, Applicants have amended claims 1 and 2 to recite that the claimed nucleic acid molecules comprise a nucleotide sequence that "hybridizes under at least moderately stringent conditions," and have amended claim 3 to delete the objected-to limitation. Applicants contend that claims 1-3, as amended, are not indefinite, and therefore, respectfully request that this ground of rejection be withdrawn.

The Action next asserts that claims 8 and 10 are indefinite for reciting the term "FGF-L polypeptide," because the specification does not identify the material element or combination of elements that is definitive of an "FGF-L polypeptide," and therefore, a skilled artisan would be

McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
Chicago, Illinois 60606
(312) 913-0001

unable to determine what additional or material limitations are placed upon a claim by the presence of this element. Applicants note first that an explicit definition of "FGF-L polypeptide" is provided in the specification at page 9, lines 21-26, and contend that this definition controls the interpretation of the term "FGF-L polypeptide" as it is used in the claims of the instant application. Applicants contend, for example, that it would be apparent to one of ordinary skill in the art that a polypeptide comprising the amino acid sequence of SEQ ID NO: 2 is a FGF-L polypeptide. Applicants further contend that it would be apparent to one of ordinary skill in the art that a polypeptide variant (*e.g.*, a polypeptide having at least one conservative amino acid substitution) of the amino acid sequence of SEQ ID NO: 2 is a FGF-L polypeptide, provided that the polypeptide variant has an activity of the polypeptide set forth in SEQ ID NO: 2. However, in order to expedite prosecution of the pending claims to allowance, and in Applicants' view because it will have no substantive effect in the proper scope of the pending claims, Applicants have amended claim 8 to recite a process of producing a polypeptide encoded by the nucleic acid molecule of any of Claims 1, 2, or 3, and have amended claim 10 to recite that the nucleic acid molecule comprises promoter DNA other than the promoter DNA for the native FGF-L gene operatively linked to the nucleic acid molecule. Applicants note that an explicit definition of the term "FGF-L gene" is provided in the specification at page 7, lines 22-26. Applicants contend, therefore, that claims 8 and 10, as amended, are not indefinite, and respectfully request that this ground of rejection be withdrawn.

The Action next asserts that claims 2-8, 10, 11, and 44 are indefinite for reciting the phrase "has an activity of the polypeptide set forth in . . . SEQ ID NO: 2," because the specification does not identify the material element or combination of elements that is definitive of an "an activity of the polypeptide set forth in . . . SEQ ID NO: 2," and therefore, a skilled artisan would be unable to determine what additional or material limitations are placed upon a claim by the presence of this element. While Applicants respectfully disagree with the assertion that this phrase is indefinite, in an effort to expedite the present application to allowance, Applicants have amended the pending claims to delete the objected-to phrase and instead affirmatively recite that FGF-L polypeptide variants or C- and/or N- terminally truncated FGF-L polypeptide variants must comprise at least 50 amino acid residues and that conservatively substituted FGF-L variants must be at least 85 percent identical to the polypeptide of SEQ ID NO: 2. Applicants contend that the claims, as amended, are not indefinite, and therefore, respectfully request that this ground of rejection be withdrawn.

McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
Chicago, Illinois 60606
(312) 913-0001

The Action next asserts that claims 1-8, 10, 11, and 44 are indefinite for reciting the term "complementary to," because it is unclear whether the claimed nucleic acid molecule is a full length complement of a recited nucleic acid molecule or complementary only to some portion of the recited nucleic acid molecule. Applicants respectfully disagree with the Action's assertion that 1-3 are indefinite for reciting the term "complementary to." Applicants contend that the nucleotide sequence complement of the nucleotide sequence 5'-A-G-C-T-A-G-C-T-3', for example, is well understood in the art to be 5'-T-C-G-A-T-C-G-A-3', rather than the nucleotide sequence 5'-T-C-G-A-T-C-G-3' or some other portion of the nucleotide sequence 5'-T-C-G-A-T-C-G-A-3'. Applicants contend, therefore, that one of ordinary skill in the art would understand that a nucleotide sequence that is complementary to the nucleotide sequence of SEQ ID NO: 1 must be the same length as the nucleotide sequence of SEQ ID NO: 1 (*i.e.*, 1330 nucleotides). Moreover, Applicants contend that such a meaning is consistent with the meaning given to the term "complementary to" by Alberts *et al.*, *Molecular Biology of the Cell*, pp. 5-7 (Garland Publishing, Inc., 1994) (describing a complementary sequence as "a mold of the original," such that the sequence of nucleotides in a nucleic acid molecule is *preserved* in its complementary strand). Applicants, therefore, respectfully contend that claims 1-3, as amended, fulfill the requirements of 35 U.S.C. § 112, first paragraph.

Applicants respectfully contend that rejections based on 35 U.S.C. § 112, second paragraph, have been overcome by amendment or traversed by argument, and request that the Examiner withdraw all rejections made on this basis.

5. Rejection of claims 1-8, 10, 11, and 44 under 35 U.S.C. § 102

The Office Action asserts a rejection of claims 3-6 and 8 under 35 U.S.C. § 102(a), as being anticipated by Koga *et al.*, 1999, *Biochem. Biophys. Res. Commun.* 261:756-65. The Action states that because the phrase "moderately or highly stringent conditions" is vague and indefinite, the nucleic acid molecule disclosed by Koga *et al.* would hybridize under moderately or highly stringent conditions to a nucleic acid molecule comprising a nucleotide sequence that is complementary to the nucleotide sequence of any of claims 3(a)-3(e). The Office Action also asserts a rejection of claims 1, 2, 4-6, 8, and 11 under 35 U.S.C. § 102(b), as being anticipated by Koga *et al.* The Action states that because the phrase "moderately or highly stringent conditions" is vague and indefinite, and Koga *et al.* disclose a nucleic acid molecule sharing a best local similarity of 74.2% with the nucleotide

McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
Chicago, Illinois 60606
(312) 913-0001

sequence of SEQ ID NO: 1, the nucleic acid molecule disclosed by Koga *et al.* would hybridize under moderately or highly stringent conditions to a nucleic acid molecule comprising a nucleotide sequence that is complementary to the nucleotide sequence of the DNA insert in ATCC Deposit No. PTA-1882. The Action also states that the nucleic acid molecule disclosed by Koga *et al.* comprises either a 16 nucleotide fragment of the nucleotide sequence of SEQ ID NO: 1 or a nucleotide sequence that is complementary to a 16 nucleotide fragment of the nucleotide sequence of SEQ ID NO: 1. The Action also states that the nucleic acid molecule disclosed by Koga *et al.* encodes a polypeptide that is at least 70% identical to the polypeptide as set forth in SEQ ID NO: 2 and comprises at least 25 amino acid residues. The Action further states that Koga *et al.* disclose a vector comprising the disclosed nucleic acid molecule, a eukaryotic host cell comprising the vector, and a process of producing the polypeptide encoded by the disclosed nucleic acid molecule comprising culturing the eukaryotic host cell.

As described in section 4 above, Applicants have amended claims 1 and 2 to recite that the claimed nucleic acid molecules comprise a nucleotide sequence that "hybridizes under at least moderately stringent conditions" to a recited nucleotide sequence. Applicants contend that claims 1 and 2, as amended, are not indefinite. In view of the specification's teachings, Applicants contend that one of ordinary skill in the art would expect nucleic acid molecules that hybridize under moderately stringent conditions to differ in their nucleotide sequences by about 21% (page 16, lines 8-9). Applicants contend, therefore, that for a nucleic acid molecule to anticipate pending claims 1(e) or 2(b), it *must* comprise a nucleotide sequence that is about 79% identical to the nucleotide sequence comprising nucleotide residues 610 through 1242 of the nucleotide sequence set forth in SEQ ID NO: 1; a nucleotide sequence encoding the polypeptide as set forth in SEQ ID NO: 2; or a nucleotide sequence of SEQ ID NO: 1 or the DNA insert in ATCC Deposit No. PTA-1882 encoding a polypeptide fragment of SEQ ID NO: 2 of at least 50 amino acid residues. As the Action suggests, even the most conserved *portion* of the nucleotide sequence disclosed by Koga *et al.* (*i.e.*, a region of 639 nucleotides) shares only 74.2% identity with the nucleotide sequence of SEQ ID NO: 1. Moreover, as shown in Exhibit F, the nucleotide sequence disclosed by Koga *et al.* shares an *overall* sequence identity of only 52.9% with the nucleotide sequence of SEQ ID NO: 1 (Exhibit F was prepared using the application MacVector 7.1.1 at the default settings). Applicants contend that because the nucleic acid molecule disclosed by Koga *et al.* could not hybridize under at least

McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
Chicago, Illinois 60606
(312) 913-0001

moderately stringent conditions to a nucleic acid molecule encompassed by the claims of the instant application, Koga *et al.* cannot anticipate claims directed to such FGF-L variants.

As described in section 3 above, Applicants have amended claims 2 and 3 so that they no longer recite an isolated nucleic acid molecule comprising either a region of the nucleotide sequence of SEQ ID NO: 1, the DNA insert in ATCC Deposit No. PTA-1882, or the nucleotide sequence of any of claims 2(a)-2(c) comprising a fragment of at least 16 nucleotides, or a nucleotide sequence of any of claims 3(a)-3(e) comprising a fragment of at least about 16 nucleotides. Applicants contend, therefore, that a 16 nucleotide fragment of the nucleotide sequence disclosed by Koga *et al.* or a nucleotide sequence that is complementary to such a fragment does not anticipate amended claims 2 and 3.

As also described in section 3 above, Applicants have amended claims 2 and 3 to recite an isolated nucleic acid molecule comprising a region of the nucleotide sequence of SEQ ID NO: 1 or the DNA insert in ATCC Deposit No. PTA-1882 encoding a polypeptide fragment of SEQ ID NO: 2 of at least 50 amino acid residues; a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 with at least one conservative amino acid substitution, wherein the encoded polypeptide is at least 85 percent identical to the polypeptide of SEQ ID NO: 2; and a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 having a C- and/or N- terminal truncation, wherein the encoded polypeptide comprises at least 50 amino acid residues. Applicants contend that the nucleotide sequence disclosed by Koga *et al.* cannot anticipate claims directed to such FGF-L variants. For the Examiner's convenience, Applicants provide a sequence comparison of the FGF-L polypeptide disclosed by Koga *et al.* and the FGF-L polypeptide disclosed in the instant application (*see* Exhibit E).

Because Koga *et al.* does not disclose a nucleotide sequence that meets each and every limitation of the claimed invention, Koga *et al. cannot* anticipate claims 1-6, 8, or 11, as amended. Applicants, therefore, respectfully request that this ground of rejection be withdrawn.

The Office Action also asserts a rejection of claims 1-8, 10, 11, and 44 under 35 U.S.C. § 102(e), as being anticipated by U.S. Patent Application Publication No. US 2002/0058036 A1 (the '036 publication), which published May 16, 2002 from U.S. Application No. 09/817,814, which was filed March 26, 2001 by Jeffers *et al*. The Action also asserts that the '036 publication is entitled to an effective filing date of July 27, 1999. The Action states that the '036 publication discloses a

McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
Chicago, Illinois 60606
(312) 913-0001

nucleic acid molecule that shares 99.8% identity with the nucleotide sequence of SEQ ID NO: 1, and that this nucleic acid molecule encodes a polypeptide that shares 100% identity with the amino acid sequence of SEQ ID NO: 2. The Action also states that the '036 publication discloses a vector comprising the disclosed nucleic acid molecule, host cells transformed with this vector, polypeptides encoded by allelic variants, nucleic acid molecules containing single nucleotide polymorphisms and encoding polypeptides containing conservative amino acid substitutions, viral vectors, promoters, enhancers, and other expression control elements, and methods of producing the polypeptide encoded by the disclosed nucleic acid molecule using prokaryotic or eukaryotic host cells.

Applicants note that U.S. Application No. 09/817,814, which was filed on March 26, 2001, and upon which the '036 publication is based, is a continuation-in-part of U.S. Application No. 09/609,543, which was filed on July 3, 2000; that U.S. Application No. 09/609,543 is a continuation-in-part of U.S. Application No. 09/494,585, which was filed on January 31, 2000; and that U.S. Application No. 09/494,585 claims the benefit of U.S. Provisional Application No. 60/145,899, which was filed on July 27, 1999. Applicants also note that while the Examiner provided a copy of the '036 publication with the instant Action, Applicants have not had access to U.S. Application Nos. 09/609,543 and 09/494,585; or U.S. Provisional Application No. 60/145,899, from which U.S. Application No. 09/817,814 claims the benefit of priority, and upon which instant rejection depends.

Applicants contend that as between the U.S. Patent Office and Applicants, the U.S. Patent Office is in the best position to demonstrate that the subject matter which forms the basis of the instant rejection (*i.e.*, the full-length nucleotide sequence of FGF-L polypeptide), and which is disclosed in U.S. Application No. 09/817,814, is (if it is) also disclosed in U.S. Application Nos. 09/609,543 and 09/494,585; and U.S. Provisional Application No. 60/145,899. Pursuant to 37 C.F.R. § 104(d)(2), Applicants request that the Examiner make a determination as to whether the full-length nucleotide sequence of FGF-L polypeptide is disclosed in U.S. Application Nos. 09/609,543 and 09/494,585; and U.S. Provisional Application No. 60/145,899. Applicants contend that in absence of such a determination, the '036 publication is only entitled to the filing date of U.S. Application No. 09/817,814 (*i.e.*, March 26, 2001), and, therefore, that this reference is not in the prior art to the instant application under 35 U.S.C. § 102. Applicants, therefore, respectfully request that this ground of rejection be withdrawn.

The Office Action also asserts a rejection of claims 1-5 and 7 under 35 U.S.C. § 102(b), as

McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
Chicago, Illinois 60606
(312) 913-0001

being anticipated by Hillier *et al.* (GenBank Accession No. AA232729). The Action states that Hillier *et al.* disclose a nucleic acid molecule that is encompassed by claims 1(d), 1(e), 2(c)-2(f), and 3(e)-3(h). The Action also states that Hillier *et al.* disclose a vector comprising the disclosed nucleic acid molecule and a prokaryotic host cell comprising the vector. The Action also states that since claim 2(c) does not specify any particular 25 amino acids and any 25 amino acid polypeptide would be antigenic, Hillier *et al.* disclose a nucleic acid molecule encoding a polypeptide fragment of at least 25 amino acid residues, wherein the polypeptide fragment is antigenic. The Action further states that claim 3(e) encompasses essentially any and all polypeptides.

As described in section 3 above, Applicants have amended claim 1 to recite an isolated nucleic acid molecule comprising a nucleotide sequence as set forth in SEQ ID NO: 1; a nucleotide sequence comprising nucleotide residues 610 through 1242 of the nucleotide sequence set forth in SEQ ID NO: 1; a nucleotide sequence of the DNA insert in ATCC Deposit No. PTA-1882; a nucleotide sequence encoding the polypeptide as set forth in SEQ ID NO: 2; a nucleotide sequence that hybridizes under at least moderately stringent conditions to the complement of a nucleotide sequence comprising nucleotide residues 610 through 1242 of the nucleotide sequence set forth in SEQ ID NO: 1 or a nucleotide sequence encoding the polypeptide as set forth in SEQ ID NO: 2; or a nucleotide sequence that is complementary to any of these nucleotide sequences. As shown in Exhibit G, while the nucleotide sequence disclosed by Hillier *et al.* comprises nucleotide residues 1 through 496 of the nucleotide sequence set forth in SEQ ID NO: 1, the FGF-L open reading frame comprises nucleotide residues 610 through 1242. Applicants contend that because the nucleotide sequence disclosed by Hillier *et al.* lacks any portion of the FGF-L open reading frame, Hillier *et al.* cannot anticipate claim 1.

As described in section 3 above, Applicants have amended claim 2 to recite an isolated nucleic acid molecule comprising a region of the nucleotide sequence of SEQ ID NO: 1 or the DNA insert in ATCC Deposit No. PTA-1882 encoding a polypeptide fragment of SEQ ID NO: 2 of at least 50 amino acid residues; a nucleotide sequence that hybridizes under at least moderately stringent conditions to the complement of this nucleotide sequence; or a nucleotide sequence that is complementary to this nucleotide sequence. Applicants contend that because amended claim 2 is directed to an isolated nucleic acid that encodes at least a portion of the FGF-L polypeptide, and the nucleotide sequence disclosed by Hillier *et al.* lacks any portion of the FGF-L open reading frame,

McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
Chicago, Illinois 60606
(312) 913-0001

Hillier *et al.* cannot anticipate claim 2.

As described in section 3 above, Applicants have amended claim 3 to recite an isolated nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 with at least one conservative amino acid substitution, wherein the encoded polypeptide is at least 85 percent identical to the polypeptide set forth in SEQ ID NO: 2; a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 having a C- and/or N- terminal truncation, wherein the encoded polypeptide comprises at least 50 amino acid residues; a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 with at least one modification that is a conservative amino acid substitution, C-terminal truncation, or N-terminal truncation, wherein the encoded polypeptide is at least 85 percent identical to the polypeptide set forth in SEQ ID NO: 2 and comprises at least 50 amino acid residues; or a nucleotide sequence that is complementary to any of these nucleotide sequences. Applicants contend that claim 3, as amended, does not encompass essentially any and all polypeptides. Applicants also contend that because amended claim 3 is directed to an isolated nucleic acid that encodes at least a portion of the FGF-L polypeptide, and the nucleotide sequence disclosed by Hillier *et al.* lacks any portion of the FGF-L open reading frame, Hillier *et al.* cannot anticipate claim 2.

Because Hillier *et al.* does not disclose a nucleotide sequence that meets each and every limitation of the claimed invention, Hillier *et al. cannot* anticipate claims 1-5 and 7, as amended. Applicants, therefore, respectfully request that this ground of rejection be withdrawn.

The Office Action also asserts a rejection of claims 3-8, 10 and 44 under 35 U.S.C. § 102(b), as being anticipated by U.S. Patent No. 5,693,775 (the '775 Patent), which issued to Nathans *et al.* on December 2, 1997. The Action states that because claim 3(e) encompasses essentially any and all polypeptides, the '775 Patent discloses a nucleic acid molecule that is encompassed by claim 3(e). The Action also states that the '775 Patent discloses a vector comprising the disclosed nucleic acid molecule, eukaryotic and prokaryotic host cells comprising the vector, and methods of making the polypeptide encoded by the disclosed nucleic acid molecule.

As described above, Applicants have amended claim 3 to recite an isolated nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 with at least one conservative amino acid substitution, wherein the encoded polypeptide is at least 85 percent identical to the polypeptide set forth in SEQ ID NO: 2; a nucleotide sequence encoding a

McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
Chicago, Illinois 60606
(312) 913-0001

polypeptide as set forth in SEQ ID NO: 2 having a C- and/or N- terminal truncation, wherein the encoded polypeptide comprises at least 50 amino acid residues; a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 with at least one modification that is a conservative amino acid substitution, C-terminal truncation, or N-terminal truncation, wherein the encoded polypeptide is at least 85 percent identical to the polypeptide set forth in SEQ ID NO: 2 and comprises at least 50 amino acid residues; or a nucleotide sequence that is complementary to any of these nucleotide sequences. Applicants contend that because claim 3, as amended, does not encompass essentially any and all polypeptides, the nucleotide sequence disclosed by Nathans *et al.* cannot anticipate claims 3-8, 10 and 44. Applicants, therefore, respectfully request that this ground of rejection be withdrawn.

Applicants respectfully contend that rejections based on 35 U.S.C. § 102 have been overcome by amendment or traversed by argument, and request that the Examiner withdraw all rejections made on this basis.

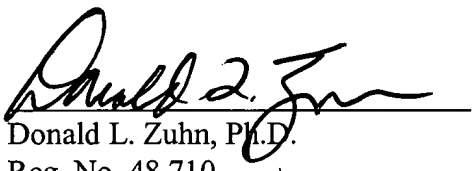
CONCLUSIONS

Applicants respectfully contend that all conditions of patentability are met in the pending claims as amended. Allowance of the claims is thereby respectfully solicited.

If Examiner Romeo believes it to be helpful, he is invited to contact the undersigned representative by telephone at 312-913-0001.

Respectfully submitted,
McDonnell Boehnen Hulbert & Berghoff

Dated: July 14, 2003

By: 
Donald L. Zuhn, Ph.D.
Reg. No. 48,710

McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
Chicago, Illinois 60606
(312) 913-0001

RJ Mazza C.S. PTO

ATCC

10801 University Blvd • Manassas, VA 20110-2209 • Telephone: 703-365-2700 • FAX: 703-365-2745

BUDAPEST TREATY ON THE INTERNATIONAL RECOGNITION OF
THE DEPOSIT OF MICROORGANISMS FOR THE PURPOSES OF PATENT PROCEDURE

INTERNATIONAL FORM

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT ISSUED PURSUANT TO RULE 7.3
AND VIABILITY STATEMENT ISSUED PURSUANT TO RULE 10.2

To: (Name and Address of Depositor or Attorney)

Amgen, Inc.
Attn: Dawn Pohl
One Amgen Center Drive, M/S 9-1-C
Thousand Oaks, CA 91320-1799

Deposited on Behalf of: Amgen, Inc.

Identification Reference by Depositor:	**Patent Deposit Designation**
Zhvt-003594, the cDNA of a human FGF-9 related molecule cloned into plasmid vector pGEM-T: JH3	PTA-1882

The deposit was accompanied by: __ a scientific description a proposed taxonomic description indicated above.

The deposit was received May 17, 2000 by this International Depository Authority and has been accepted.

AT YOUR REQUEST: X We will inform you of requests for the strain for 30 years.

The strain will be made available if a patent office signatory to the Budapest Treaty certifies one's right to receive, or if a U.S. Patent is issued citing the strain, and ATCC is instructed by the United States Patent & Trademark Office or the depositor to release said strain.

If the culture should die or be destroyed during the effective term of the deposit, it shall be your responsibility to replace it with living culture of the same.

The strain will be maintained for a period of at least 30 years from date of deposit, or five years after the most recent request for a sample, whichever is longer. The United States and many other countries are signatory to the Budapest Treaty.

The viability of the culture cited above was tested May 25, 2000. On that date, the culture was viable.

International Depository Authority: American Type Culture Collection, Manassas, VA 20110-2209 USA.

Signature of person having authority to represent ATCC:

Date: May 30, 2000

Barbara E. Coupé, Administrator, Patent Depository

cc: Richard J. Mazza (Ref: Docket or Case No.: A-668-P)

EXHIBIT A

```
                10         20         30         40         50
SEQ 1      TACACGGCCGCAGCTGAACAGCATCACCGCTGTCCCAAGGACAACCCCAA
           ATGTGCCGGCGTCGACTTGTCGTAGTGGCGACAGGGTTCCTGTTGGGGTT

                60         70         80         90        100
SEQ 1      AGAGGGGCCTCGACTGCACCTCCTCGAAGTTGCTGGCTGGCTTTGGCAAG
           TCTCCCCGGAGCTGACGTGGAGGAGCTTCAACGACCGACCGAAACCGTTC

               110        120        130        140        150
SEQ 1      TGCAGGAATGGTGTTTTGTGAGGGCATGGATGGAGAAGTGCCAAGGGCCC
           ACGTCCTTACCACAAAACACTCCCGTACCTACCTCTTCACGGTTCCCGGG

               160        170        180        190        200
SEQ 1      CTGTTTGGTCACTTCCGAAGAGCAAAAACGTGTTGAGAGGAGACCGGTTT
           GACAAACCAGTGAAGGCTTCTCGTTTTTGCACAACTCTCCTCTGGCCAAA

               210        220        230        240        250
SEQ 1      AAGATTTCAAACAGAACCTCCCCAGCGCGCATGAAAGGACTTGATTAGCA
           TTCTAAAGTTTGTCTTGGAGGGGTCGCGCGTACTTTCCTGAACTAATCGT

               260        270        280        290        300
SEQ 1      TATGTCAAGAGGACCCGCTTATATACTCGGTGTGTATGTACACAGGACTC
           ATACAGTTCTCCTGGGCGAATATATGAGCCACACATACATGTGTCCTGAG

               310        320        330        340        350
SEQ 1      TGATCTGATCAGTTTGCGGAATTGGAGCCCCAGCCAACAGCCCTAGTCCT
           ACTAGACTAGTCAAACGCCTTAACCTCGGGGTCGGTTGTCGGGATCAGGA

               360        370        380        390        400
SEQ 1      AGTATTGGCAGCGGCAGCTATAGATATTTCTGCAGAGCCAGCAGCCGGCT
           TCATAACCGTCGCCGTCGATATCTATAAAGACGTCTCGGTCGTCGGCCGA

               410        420        430        440        450
SEQ 1      CCCACCTACCCAAGGAGAGAAGATCGCTCCAAGACAGTGAGAGCTTCCCT
           GGGTGGATGGGTTCCTCTCTTCTAGCGAGGTTCTGTCACTCTCGAAGGGA

               460        470        480        490        500
SEQ 1      GCCATTTCAGTGCAAAGTCCCTCCGGAGCGACCTCAGAGGAGTAACCGGG
           CGGTAAAGTCACGTTTCAGGGAGGCCTCGCTGGAGTCTCCTCATTGGCCC

               510        520        530        540        550
SEQ 1      CCTTAACTTTTTGCGCTCGTTTTGCTATAATTTTTCTCTATCCACCTCCA
           GGAATTGAAAAACGCGAGCAAAACGATATTAAAAAGAGATAGGTGGAGGT
```

```
                560        570        580        590        600
SEQ 1       TCCCACCCCCACAACACTCTTTACTGGGGGGGTCTTTTGTGTTCCGGATC
            AGGGTGGGGGTGTTGTGAGAAATGACCCCCCCAGAAAACACAAGGCCTAG

                610        620        630        640        650
SEQ 1       TCCCCCTCCATGGCTCCCTTAGCCGAAGTCGGGGGCTTTCTGGGCGGCCT
            AGGGGGAGGTACCGAGGGAATCGGCTTCAGCCCCCGAAAGACCCGCCGGA

1. FIG. 1                   10         20         30         40
[ 2532 ]              ATGGCTCCCTTAGCCGAAGTCGGGGGCTTTCTGGGCGGCCT>
                      ||||||||||||||||||||||||||||||||||||||||
SEQ 1                 ATGGCTCCCTTAGCCGAAGTCGGGGGCTTTCTGGGCGGCCT

                660        670        680        690        700
SEQ 1       GGAGGGCTTGGGCCAGCAGGTGGGTTCGCATTTCCTGTTGCCTCCTGCCG
            CCTCCCGAACCCGGTCGTCCACCCAAGCGTAAAGGACAACGGAGGACGGC

1. FIG. 1          50         60         70         80         90
[ 2532 ]     GGAGGGCTTGGGCCAGCAGGTGGGTTCGCATTTCCTGTTGCCTCCTGCCG>
             ||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ 1        GGAGGGCTTGGGCCAGCAGGTGGGTTCGCATTTCCTGTTGCCTCCTGCCG

                710        720        730        740        750
SEQ 1       GGGAGCGGCCGCCGCTGCTGGGCGAGCGCAGGAGCGCGGCGGAGCGGAGC
            CCCTCGCCGGCGGCGACGACCCGCTCGCGTCCTCGCGCCGCCTCGCCTCG

1. FIG. 1         100        110        120        130        140
[ 2532 ]     GGGAGCGGCCGCCGCTGCTGGGCGAGCGCAGGAGCGCGGCGGAGCGGAGC>
             ||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ 1        GGGAGCGGCCGCCGCTGCTGGGCGAGCGCAGGAGCGCGGCGGAGCGGAGC

                760        770        780        790        800
SEQ 1       GCCCGCGGCGGGCCGGGGGCTGCGCAGCTGGCGCACCTGCACGGCATCCT
            CGGGCGCCGCCCGGCCCCCGACGCGTCGACCGCGTGGACGTGCCGTAGGA

1. FIG. 1         150        160        170        180        190
[ 2532 ]     GCCCGCGGCGGGCCGGGGGCTGCGCAGCTGGCGCACCTGCACGGCATCCT>
             ||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ 1        GCCCGCGGCGGGCCGGGGGCTGCGCAGCTGGCGCACCTGCACGGCATCCT

                810        820        830        840        850
SEQ 1       GCGCCGCCGGCAGCTCTATTGCCGCACCGGCTTCCACCTGCAGATCCTGC
            CGCGGCGGCCGTCGAGATAACGGCGTGGCCGAAGGTGGACGTCTAGGACG

1. FIG. 1         200        210        220        230        240
[ 2532 ]     GCGCCGCCGGCAGCTCTATTGCCGCACCGGCTTCCACCTGCAGATCCTGC>
             ||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ 1        GCGCCGCCGGCAGCTCTATTGCCGCACCGGCTTCCACCTGCAGATCCTGC
```

```
                860        870        880        890        900
SEQ 1           CCGACGGCAGCGTGCAGGGCACCCGGCAGGACCACAGCCTCTTCGGTATC
                GGCTGCCGTCGCACGTCCCGTGGGCCGTCCTGGTGTCGGAGAAGCCATAG

1. FIG. 1          250        260        270        280        290
[ 2532 ]        CCGACGGCAGCGTGCAGGGCACCCGGCAGGACCACAGCCTCTTCGGTATC>
                ||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ 1           CCGACGGCAGCGTGCAGGGCACCCGGCAGGACCACAGCCTCTTCGGTATC


                910        920        930        940        950
SEQ 1           TTGGAATTCATCAGTGTGGCAGTGGGACTGGTCAGTATTAGAGGTGTGGA
                AACCTTAAGTAGTCACACCGTCACCCTGACCAGTCATAATCTCCACACCT

1. FIG. 1          300        310        320        330        340
[ 2532 ]        TTGGAATTCATCAGTGTGGCAGTGGGACTGGTCAGTATTAGAGGTGTGGA>
                ||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ 1           TTGGAATTCATCAGTGTGGCAGTGGGACTGGTCAGTATTAGAGGTGTGGA


                960        970        980        990       1000
SEQ 1           CAGTGGTCTCTATCTTGGAATGAATGACAAAGGAGAACTCTATGGATCAG
                GTCACCAGAGATAGAACCTTACTTACTGTTTCCTCTTGAGATACCTAGTC

1. FIG. 1          350        360        370        380        390
[ 2532 ]        CAGTGGTCTCTATCTTGGAATGAATGACAAAGGAGAACTCTATGGATCAG>
                ||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ 1           CAGTGGTCTCTATCTTGGAATGAATGACAAAGGAGAACTCTATGGATCAG


               1010       1020       1030       1040       1050
SEQ 1           AGAAACTTACTTCCGAATGCATCTTTAGGGAGCAGTTTGAAGAGAACTGG
                TCTTTGAATGAAGGCTTACGTAGAAATCCCTCGTCAAACTTCTCTTGACC

1. FIG. 1          400        410        420        430        440
[ 2532 ]        AGAAACTTACTTCCGAATGCATCTTTAGGGAGCAGTTTGAAGAGAACTGG>
                ||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ 1           AGAAACTTACTTCCGAATGCATCTTTAGGGAGCAGTTTGAAGAGAACTGG


               1060       1070       1080       1090       1100
SEQ 1           TATAACACCTATTCATCTAACATATATAAACATGGAGACACTGGCCGCAG
                ATATTGTGGATAAGTAGATTGTATATATTTGTACCTCTGTGACCGGCGTC

1. FIG. 1          450        460        470        480        490
[ 2532 ]        TATAACACCTATTCATCTAACATATATAAACATGGAGACACTGGCCGCAG>
                ||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ 1           TATAACACCTATTCATCTAACATATATAAACATGGAGACACTGGCCGCAG


               1110       1120       1130       1140       1150
SEQ 1           GTATTTTGTGGCACTTAACAAAGACGGAACTCCAAGAGATGGCGCCAGGT
                CATAAAACACCGTGAATTGTTTCTGCCTTGAGGTTCTCTACCGCGGTCCA
```

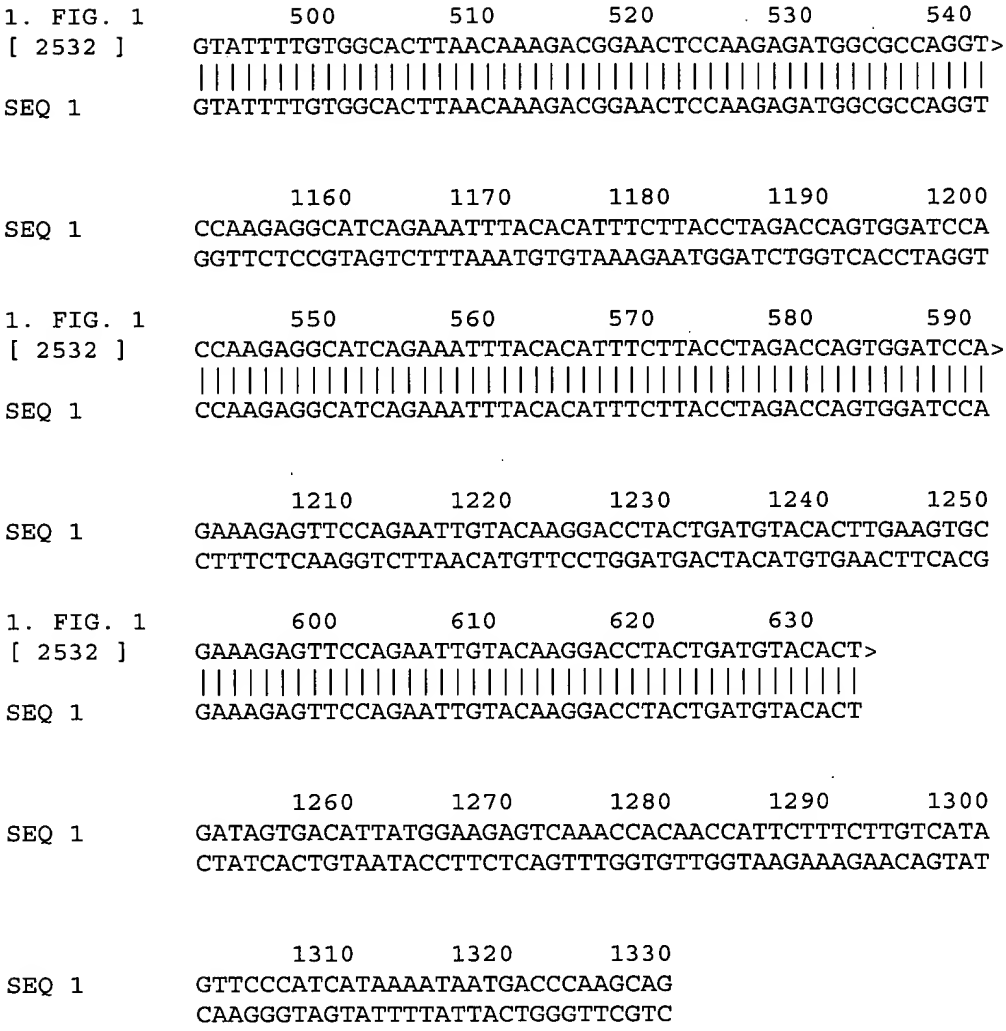

1. FIG. 1
500 510 520 530 540
[2532]
GTATTTTGTGGCACTTAACAAAGACGGAACTCCAAGAGATGGCGCCAGGT>
SEQ 1
GTATTTTGTGGCACTTAACAAAGACGGAACTCCAAGAGATGGCGCCAGGT
1160 1170 1180 1190 1200
SEQ 1
CCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATCCA
GGTTCTCCGTAGTCTTTAAATGTGTAAAGAATGGATCTGGTCACCTAGGT
1. FIG. 1
550 560 570 580 590
[2532]
CCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATCCA>
SEQ 1
CCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATCCA
1210 1220 1230 1240 1250
SEQ 1
GAAAGAGTTCCAGAATTGTACAAGGACCTACTGATGTACACTTGAAGTGC
CTTTCTCAAGGTCTTAACATGTTCCTGGATGACTACATGTGAACTTCACG
1. FIG. 1
600 610 620 630
[2532]
GAAAGAGTTCCAGAATTGTACAAGGACCTACTGATGTACACT>
SEQ 1
GAAAGAGTTCCAGAATTGTACAAGGACCTACTGATGTACACT
1260 1270 1280 1290 1300
SEQ 1
GATAGTGACATTATGGAAGAGTCAAACCACAACCATTCTTTCTTGTCATA
CTATCACTGTAATACCTTCTCAGTTTGGTGTTGGTAAGAAAGAACAGTAT
1310 1320 1330
SEQ 1
GTTCCCATCATAAAATAATGACCCAAGCAG
CAAGGGTAGTATTTTATTACTGGGTTCGTC

EXHIBIT B

```
Aligned Length = 212   Gaps = 2
Identities = 144 (68%)   Similarities = 26 (12%)

huFGF-L     1 MAPLAEVGGFLGGLEGLGQQVGSHFLLPPAGERPPLLGERRSAAER-SAR  49
FGF-9       1 MAPLGEVGNYFGVQDAVPFGNVPVLP----VDSPVLLSDHLGQSEAGGLP  46
              **** ***.. *  . .               . * ** ..   .*

huFGF-L    50 GGPGAAQLAHLHGILRRRQLYCRTGFHLQILPDGSVQGTRQDHSLFGILE  99
FGF-9      47 RGPAVTDLDHLKGILRRRQLYCRTGFHLEIFPNGTIQGTRKDHSRFGILE  96
               **  . * **.****************.* * *..****.*** *****

huFGF-L   100 FISVAVGLVSIRGVDSGLYLGMNDKGELYGSEKLTSECIFREQFEENWYN 149
FGF-9      97 FISIAVGLVSIRGVDSGLYLGMNEKGELYGSEKLTQECVFREQFEENWYN 146
              ***.******************.*********** **.***********

huFGF-L   150 TYSSNIYKHGDTGRRYFVALNKDGTPRDGARSKRHQKFTHFLPRPVDPER 199
FGF-9     147 TYSSNLYKHVDTGRRYYVALNKDGTPREGTRTKRHQKFTHFLPRPVDPDK 196
              *****.*** ******.**********.*.*.****************..

huFGF-L   200 VPELYKDLLMYT 211
FGF-9     197 VPELYKDILSQS 208
              *******.*  .
```

```
Aligned Length = 211   Gaps = 1
Identities = 131 (62%)   Similarities = 30 (14%)

huFGF-L     1 MAPLAEVGGFLGGLEGLGQQVGSHFLLPPAGERPPLLGERRSAAERSARG  50
FGF-16      1    MAEVGGVFASLDWDLHGFSSSLGNVPLADSPGFLNERLGQIEGKLQR  47
               .*****    *.   .   *     *  . *  *.**    *   .

huFGF-L    51 GPGAAQLAHLHGILRRRQLYCRTGFHLQILPDGSVQGTRQDHSLFGILEF 100
FGF-16     48 G-SPTDFAHLKGILRRRQLYCRTGFHLEIFPNGTVHGTRHDHSRFGILEF  96
              *   .  ***.****************.* * *.*.***.*** ******

huFGF-L   101 ISVAVGLVSIRGVDSGLYLGMNDKGELYGSEKLTSECIFREQFEENWYNT 150
FGF-16     97 ISLAVGLISIRGVDSGLYLGMNERGELYGSKKLTRECVFREQFEENWYNT 146
              **.****.**************..****** *** **.************

huFGF-L   151 YSSNIYKHGDTGRRYFVALNKDGTPRDGARSKRHQKFTHFLPRPVDPERV 200
FGF-16    147 YASTLYKHSDSERQYYVALNKDGSPREGYRTKRHQKFTHFLPRPVDPSKL 196
              *.*..*** *. *.*.*******.**.* *.***************** ..

huFGF-L   201 PELYKDLLMYT 211
FGF-16    197 PSMSRDLFHYR 207
              * . .**  *
```

Exhibit C

ClustalW (v1.4) Multiple Alignment Parameters:
Open Gap Penalty = 10.0; Extend Gap Penalty = 0.0; Delay Divergent = 40%
Gap Distance = 8; Similarity Matrix = blosum

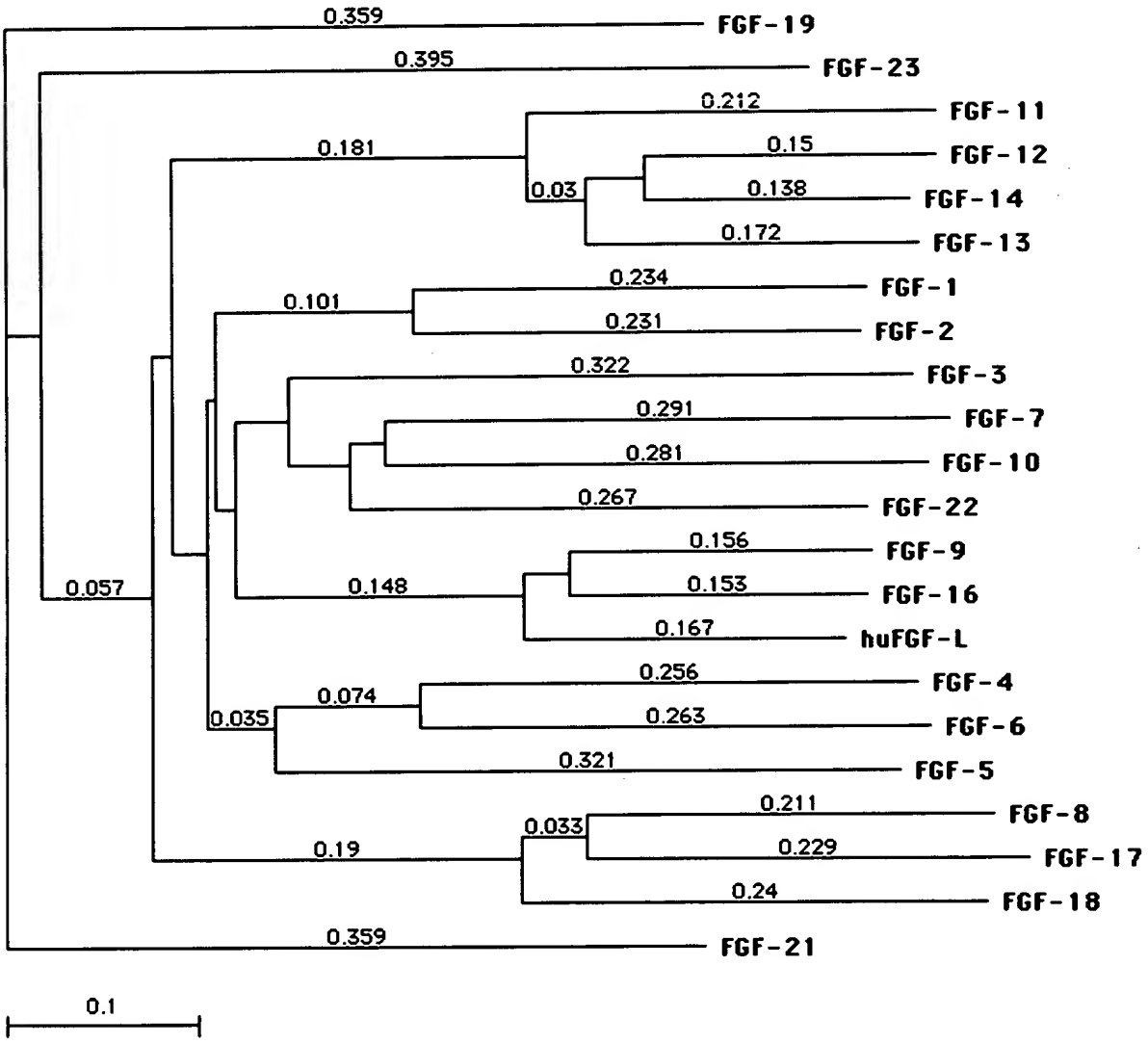


EXHIBIT D

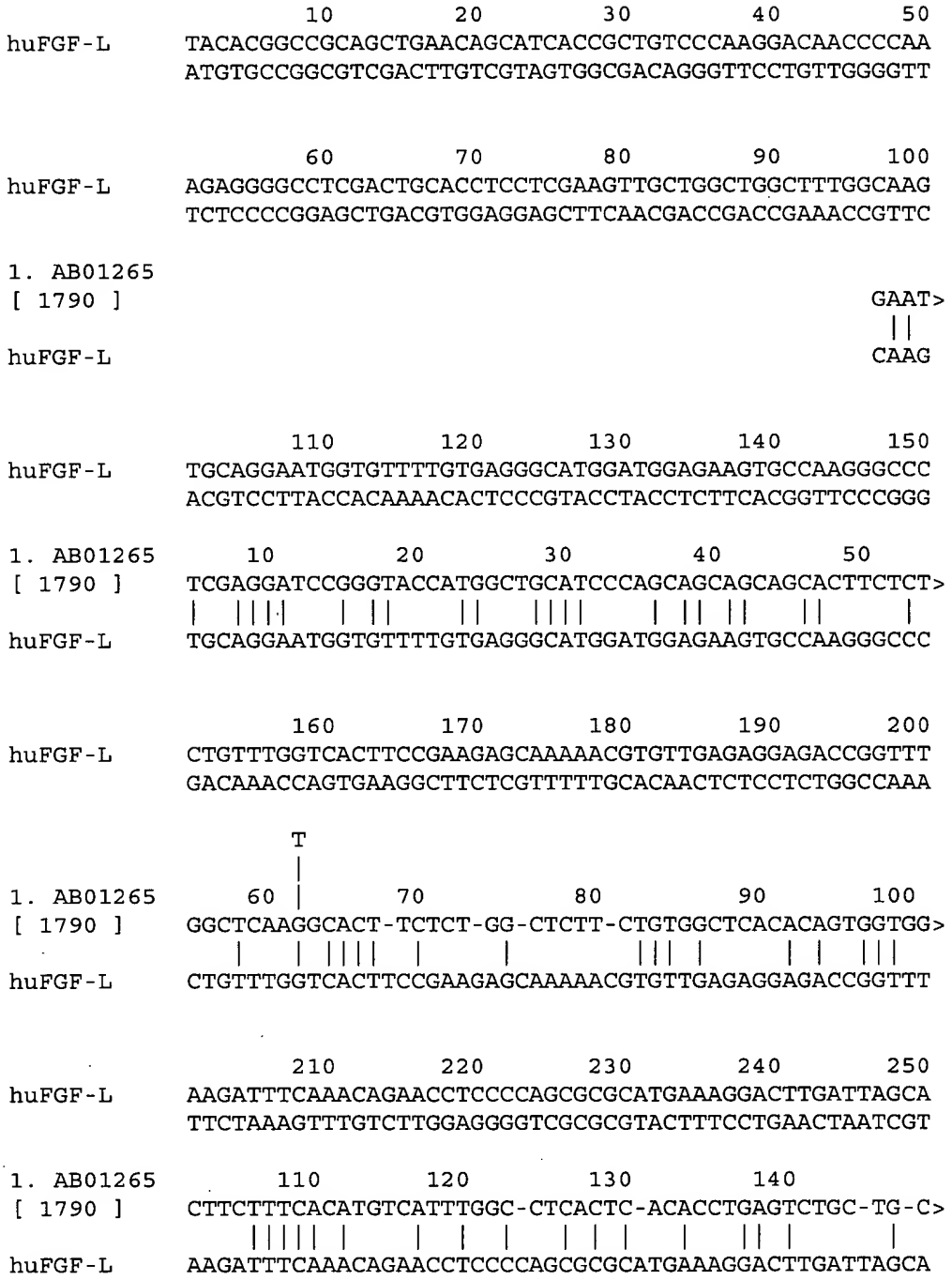
Sequences producing significant alignments:	Score (bits)	E Value
gi|9789947|ref|NP_062825.1| fibroblast growth factor 20 [Ho...	345	2e-94
gi|26342460|dbj|BAC34892.1| unnamed protein product [Mus mu...	341	4e-93
gi|13027408|ref|NP_076451.1| fibroblast growth factor 20 [R...	337	8e-92
gi|13447396|ref|NP_085113.1| fibroblast growth factor 20 [M...	337	1e-91
gi|7512161|pir||JC7082 fibroblast somatotropin-20 - African...	**304**	**5e-82**
gi|2494456|sp|Q91875|FGF9_XENLA GLIA-ACTIVATING FACTOR PREC...	**283**	**9e-76**
gi|30038758|dbj|BAC75716.1| fibroblast groth factor 9 [Gall...	281	4e-75
gi|4503707|ref|NP_002001.1| fibroblast growth factor 9 prec...	279	2e-74
gi|7305057|ref|NP_038546.1| fibroblast growth factor 9; gli...	279	2e-74
gi|13399478|pdb|1G82|A Chain A, Structure Of Fibroblast Gro...	**279**	**3e-74**
gi|25742766|ref|NP_037084.1| fibroblast growth factor 9 [Ra...	279	3e-74
gi|15487681|gb|AAK61609.2| fibroblast growth factor 9 [Sus ...	278	4e-74
gi|14278240|pdb|1IHK|A Chain A, Crystal Structure Of Fibrob...	277	7e-74
gi|11093923|gb|AAG29501.1| FGF-16 protein [Mus musculus]	**254**	**8e-67**
gi|4503691|ref|NP_003859.1| fibroblast growth factor 16 [Ho...	253	1e-66
gi|11177916|ref|NP_068639.1| fibroblast growth factor 16 [R...	253	1e-66
gi|13449275|ref|NP_085117.1| fibroblast growth factor 16 [M...	251	6e-66
gi|19912822|dbj|BAB88673.1| fibroblast growth factor 9/16/2...	140	1e-32
gi|24137641|dbj|BAC22069.1| fibroblast growth factor 9/16/2...	137	9e-32
gi|19031193|gb|AAK59700.1| fibroblast growth factor 10 [Amb...	129	3e-29
gi|6911123|gb|AAF31393.1|AF199606_1 fibroblast growth facto...	**126**	**2e-28**
gi|1345995|sp|P48801|FGF3_CHICK Fibroblast growth factor-3 ...	126	3e-28
gi|28872756|ref|NP_787125.1| fibroblast growth factor 14 is...	125	6e-28
gi|2911146|dbj|BAA24945.1| fibroblast growth factor 10 [Gal...	**124**	**7e-28**
gi|3299784|dbj|BAA31543.1| FHF-4b [Mus musculus] >gi|329978...	**124**	**7e-28**
gi|19070525|gb|AAL83904.1|AF348523_1 fibroblast growth fact...	124	8e-28
gi|4758368|ref|NP_004106.1| fibroblast growth factor 14 iso...	124	9e-28
gi|19224657|ref|NP_071559.2| fibroblast growth factor 14; F...	124	9e-28
gi|6911121|gb|AAF31392.1|AF199605_1 fibroblast growth facto...	**124**	**1e-27**
gi|4758360|ref|NP_004456.1| fibroblast growth factor 10 pre...	124	1e-27
gi|6978837|ref|NP_037083.1| fibroblast growth factor 10 [Ra...	124	1e-27
gi|14388499|dbj|BAB60779.1| hypothetical protein [Macaca fa...	124	1e-27
gi|6753848|ref|NP_034331.1| fibroblast growth factor 14 [Mu...	124	1e-27
gi|21314400|gb|AAM46926.1|AF508782_1 fibroblast growth fact...	123	2e-27
gi|28949024|pdb|1NUN|A Chain A, Crystal Structure Analysis ...	122	3e-27
gi|544288|sp|P36386|FGF3_XENLA FIBROBLAST GROWTH FACTOR-3 P...	**122**	**4e-27**
gi|7106313|ref|NP_032028.1| fibroblast growth factor 10 [Mu...	122	5e-27
gi|18543363|ref|NP_570107.1| fibroblast growth factor 22 [R...	121	7e-27
gi|69035|pir||TVHUF5 fibroblast growth factor 5 - human >gi...	**121**	**7e-27**
gi|11559990|ref|NP_071547.1| fibroblast growth factor FGF-5...	121	7e-27
gi|4758370|ref|NP_004455.1| fibroblast growth factor 5 isof...	121	8e-27
gi|22655537|gb|AAN04097.1| fibroblast growth factor-5 [Homo...	121	8e-27
gi|6753854|ref|NP_034333.1| fibroblast growth factor 5 [Mus...	121	9e-27
gi|6708457|gb|AAF25944.1|AF213396_1 fibroblast growth facto...	**121**	**9e-27**
gi|13637763|sp|P12034|FGF5_HUMAN Fibroblast growth factor-5...	121	9e-27
gi|4512022|gb|AAD21576.1| fibroblast growth factor 13 isofo...	**120**	**1e-26**
gi|15705915|gb|AAL05875.1|AF411527_1 keratinocyte growth fa...	120	2e-26
gi|13626683|sp|P79150|FGF7_CANFA Keratinocyte growth factor...	120	2e-26
gi|31542809|ref|NP_034330.2| fibroblast growth factor 13 [M...	119	3e-26
gi|2494462|sp|P70377|FGFD_MOUSE FIBROBLAST GROWTH FACTOR-13...	**119**	**3e-26**
gi|4758366|ref|NP_004105.1| fibroblast growth factor 13 iso...	119	3e-26

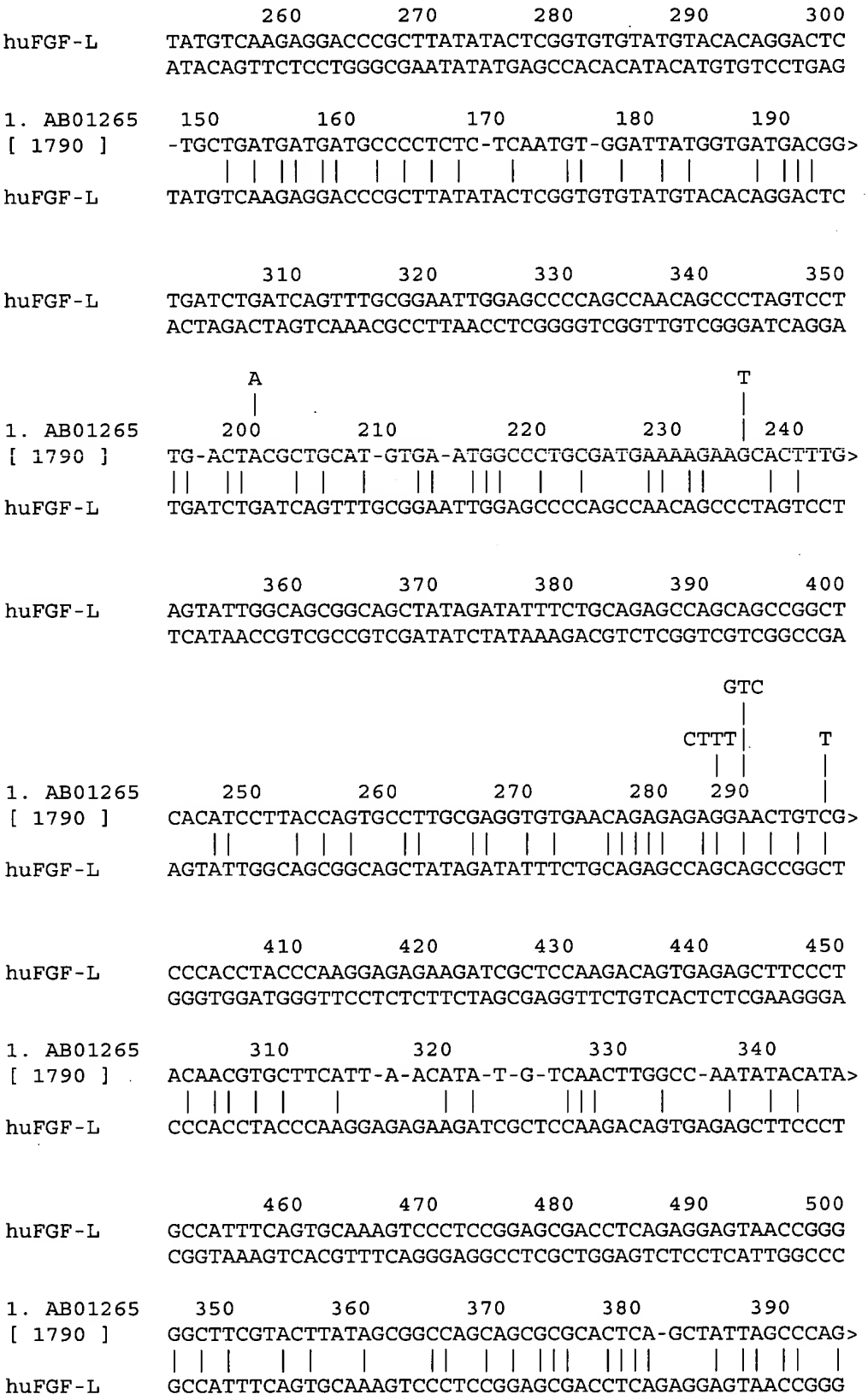
gi|4503705|ref|NP_002000.1| fibroblast growth factor 7 prec...	119	3e-26
gi|430968|gb|AAA67335.1| human keratinocyte growth factor	**119**	**3e-26**
gi|2444477|gb|AAB71606.1| fibroblast growth factor-related ...	**119**	**3e-26**
gi|6911131|gb|AAF31397.1|AF199610_1 fibroblast growth facto...	**119**	**4e-26**
gi|1346000|sp|P48808|FGF7_SHEEP KERATINOCYTE GROWTH FACTOR ...	**119**	**4e-26**
gi|12963627|ref|NP_075793.1| fibroblast growth factor 22 [M...	118	6e-26
gi|28191242|gb|AAO33291.1| fibroblast growth factor-like pr...	118	6e-26
gi|16758168|ref|NP_445880.1| fibroblast growth factor 13 [R...	117	1e-25
gi|18677745|ref|NP_570830.1| fibroblast growth factor 3 [Ra...	117	2e-25
gi|16306543|ref|NP_378668.1| fibroblast growth factor 13 is...	117	2e-25
gi|6679783|ref|NP_032033.1| fibroblast growth factor 3 [Mus...	116	3e-25
gi|18490696|gb|AAH22524.1| Unknown (protein for MGC:26659) ...	115	4e-25
gi|21614511|ref|NP_004104.3| fibroblast growth factor 12 is...	115	5e-25
gi|4885233|ref|NP_005238.1| fibroblast growth factor 3 prec...	115	5e-25
gi|13626616|sp|Q9N198|FGF7_PIG Keratinocyte growth factor p...	115	7e-25
gi|11136630|ref|NP_066360.1| fibroblast growth factor 12 is...	115	7e-25
gi|6911116|gb|AAF31390.1|AF199602_1 fibroblast growth facto...	**114**	**7e-25**
gi|18677741|ref|NP_570827.1| fibroblast growth factor 12; f...	114	7e-25
gi|2444479|gb|AAB71607.1| fibroblast growth factor-related ...	**114**	**8e-25**
gi|4512020|gb|AAD21575.1| fibroblast growth factor 12 isofo...	**114**	**1e-24**
gi|7438523|pir||JG0184 fibroblast growth factor - human	**114**	**1e-24**
gi|5442453|gb|AAB18786.3| fibroblast growth factor [Homo sa...	**112**	**4e-24**
gi|16305071|gb|AAL16959.1|AF360986_1 fibroblast growth fact...	112	4e-24
gi|6980587|pdb|1QQL|A Chain A, The Crystal Structure Of Fib...	**112**	**5e-24**
gi|1749791|emb|CAA94240.1| fibroblast growth factor 12 [Hom...	**112**	**5e-24**
gi|18858671|ref|NP_571366.1| fibroblast growth factor 3 [Da...	110	1e-23
gi|16226033|gb|AAL16059.1| keratinocyte growth factor FGF-7...	110	1e-23
gi|7438522|pir||S26049 fibroblast growth factor 7 precursor...	**108**	**7e-23**
gi|27464175|gb|AAO15997.1| fibroblast growth factor 6 [Dani...	108	8e-23
gi|25396669|pir||H88481 protein let-756 [imported] - Caenor...	107	1e-22
gi|3980190|emb|CAA76422.1| fibroblast growth factor 6-relat...	**107**	**2e-22**
gi|1346001|sp|P48805|FGFA_XENLA Fibroblast growth factor-4-...	107	2e-22
gi|1749789|emb|CAA94239.1| fibroblast growth factor 11 [Hom...	**107**	**2e-22**
gi|11559943|ref|NP_071518.1| fibroblast growth factor 7 [Ra...	107	2e-22
gi|6679785|ref|NP_032034.1| fibroblast growth factor 7; Ker...	106	2e-22
gi|6980585|pdb|1QQK|A Chain A, The Crystal Structure Of Fib...	**106**	**2e-22**
gi|16305079|gb|AAL16963.1|AF360990_1 fibroblast growth fact...	106	3e-22
gi|6714538|dbj|BAA89483.1| FGF-14C (FHF-4C) [Mus musculus]	**105**	**4e-22**
gi|4758362|ref|NP_004103.1| fibroblast growth factor 11; fi...	105	4e-22
gi|15147343|ref|NP_066276.2| fibroblast growth factor 6 pre...	105	5e-22
gi|32491|emb|CAA45054.1| hst-2 (FGF-6) [Homo sapiens]	**105**	**7e-22**
gi|18677743|ref|NP_570829.1| fibroblast growth factor 11 [R...	104	1e-21
gi|6753844|ref|NP_034328.1| fibroblast growth factor 11 [Mu...	104	1e-21
gi|18858673|ref|NP_571710.1| fibroblast growth factor 4 [Da...	104	1e-21
gi|24137647|dbj|BAC22072.1| fibroblast growth factor 11/12/...	103	1e-21
gi|24571204|gb|AAN62915.1| fibroblast growth factor 10 [Dan...	103	2e-21
gi|18777759|ref|NP_571983.1| fibroblast growth factor 6 [Ra...	103	2e-21
gi|1346002|sp|P48806|FGFB_XENLA Fibroblast growth factor-4-...	103	2e-21
gi|17554196|ref|NP_498403.1| Lethal-756, essential fibrobla...	102	3e-21

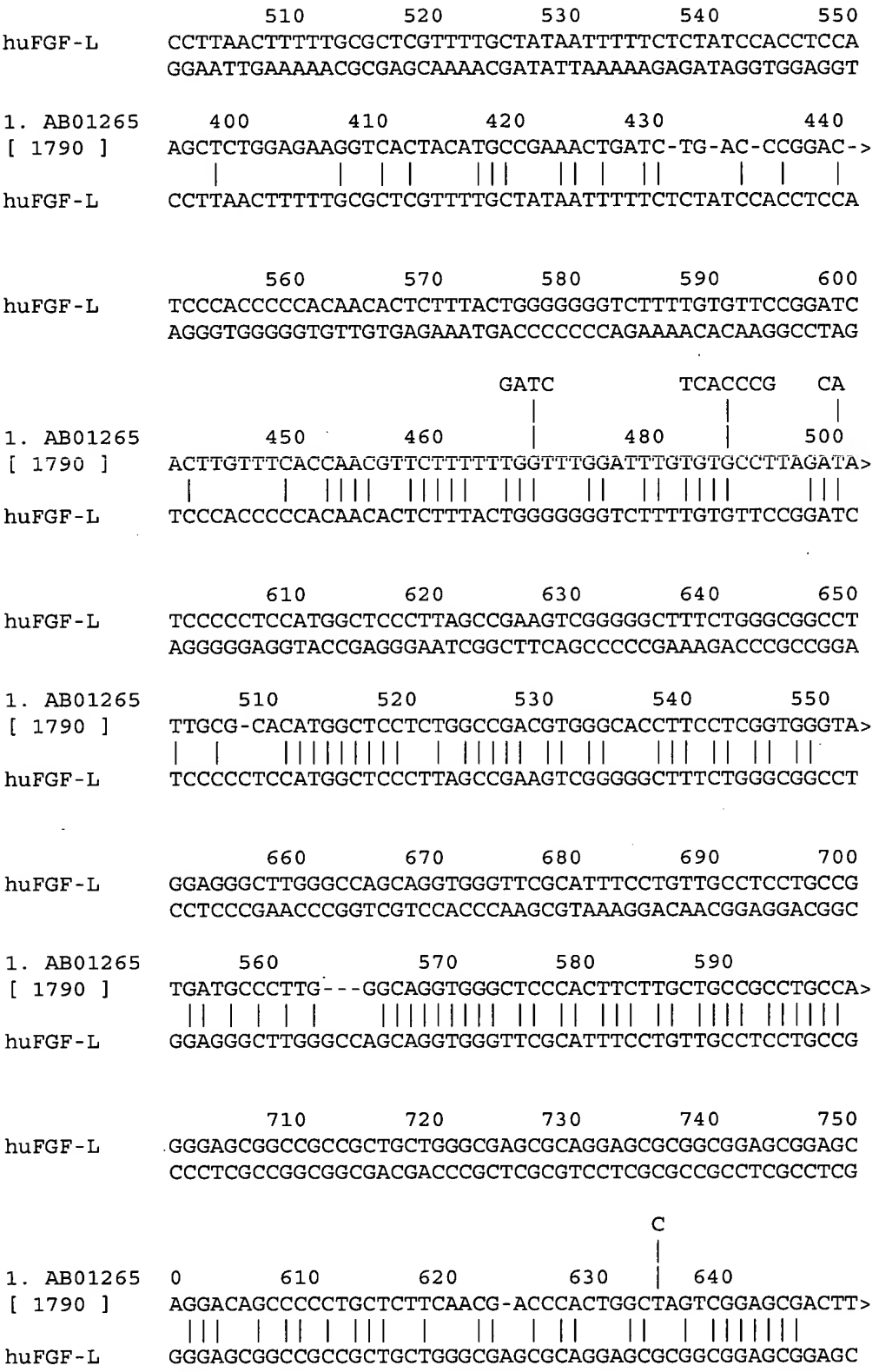
EXHIBIT E

```
Aligned Length = 211   Gaps = 2
Identities = 170 (80%)   Similarities = 21 (9%)

huFGF-L AA     1 MAPLAEVGGFLGGLEGLGQQVGSHFLLPPAGERPPLLGERRSAAERSARG  50
AB01265_AA     1 MAPLADVGTFLGGYDALG-QVGSHFLLPPAKDSPLLFNDPLAQSERLSRS  49
                 *****.** **** . ** ********** . * * .. . .** .*

huFGF-L AA    51 GPGAAQLAHLHGILRRRQLYCRTGFHLQILPDGSVQGTRQDHSLFGILEF 100
AB01265_AA    50 AP--SDLSHLQGILRRRQLYCRTGFHLQILPDGNVQGTRQDHSRFGILEF  97
                  *  . *.**.********************** ********* ******

huFGF-L AA   101 ISVAVGLVSIRGVDSGLYLGMNDKGELYGSEKLTSECIFREQFEENWYNT 150
AB01265_AA    98 ISVAIGLVSIRGVDTGLYLGMNDKGELFGSEKLTSECIFREQFEENWYNT 147
                 ****.*********.************.**********************

huFGF-L AA   151 YSSNIYKHGDTGRRYFVALNKDGTPRDGARSKRHQKFTHFLPRPVDPERV 200
AB01265_AA   148 YSSNLYKHGDSGRRYFVALNKDGTPRDGTRAKRHQKFTHFLPRPVDPEKV 197
                 ****.*****.*****************.*.*****************.*

huFGF-L AA   201 PELYKDLLMYT 211
AB01265_AA   198 PELYKDLMGYS 208
                 *******. *.
```

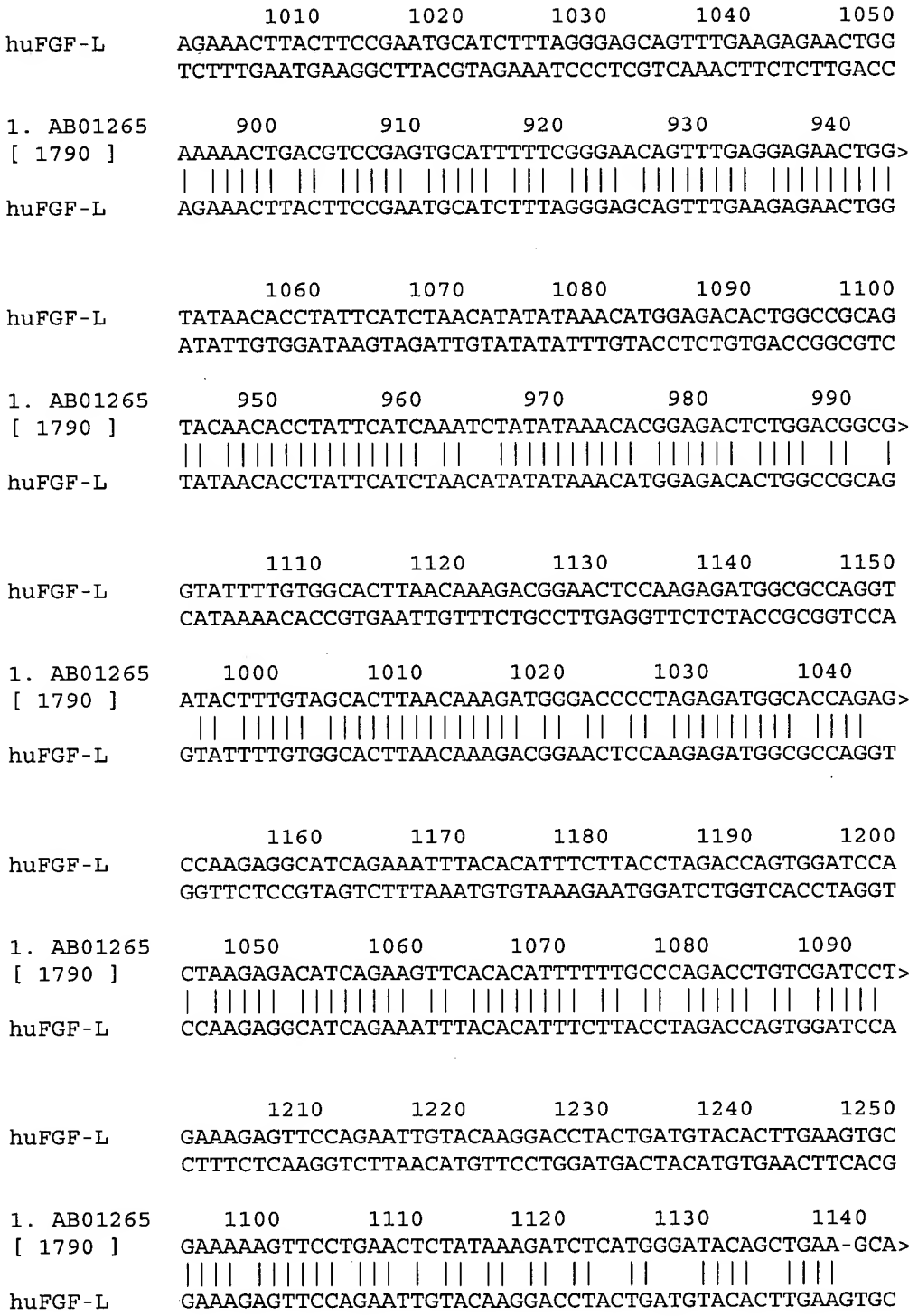
EXHIBIT F


10 20 30 40 50
huFGF-L TACACGGCCGCAGCTGAACAGCATCACCGCTGTCCCAAGGACAACCCCAA
ATGTGCCGGCGTCGACTTGTCGTAGTGGCGACAGGGTTCCTGTTGGGGTT
60 70 80 90 100
huFGF-L AGAGGGGCCTCGACTGCACCTCCTCGAAGTTGCTGGCTGGCTTTGGCAAG
TCTCCCCGGAGCTGACGTGGAGGAGCTTCAACGACCGACCGAAACCGTTC
1. AB01265
[1790] GAAT>
huFGF-L CAAG
110 120 130 140 150
huFGF-L TGCAGGAATGGTGTTTTGTGAGGGCATGGATGGAGAAGTGCCAAGGGCCC
ACGTCCTTACCACAAAACACTCCCGTACCTACCTCTTCACGGTTCCCGGG
1. AB01265 10 20 30 40 50
[1790] TCGAGGATCCGGGTACCATGGCTGCATCCCAGCAGCAGCAGCACTTCTCT>
huFGF-L TGCAGGAATGGTGTTTTGTGAGGGCATGGATGGAGAAGTGCCAAGGGCCC
160 170 180 190 200
huFGF-L CTGTTTGGTCACTTCCGAAGAGCAAAAACGTGTTGAGAGGAGACCGGTTT
GACAAACCAGTGAAGGCTTCTCGTTTTTGCACAACTCTCCTCTGGCCAAA
T
1. AB01265 60 70 80 90 100
[1790] GGCTCAAGGCACT-TCTCT-GG-CTCTT-CTGTGGCTCACACAGTGGTGG>
huFGF-L CTGTTTGGTCACTTCCGAAGAGCAAAAACGTGTTGAGAGGAGACCGGTTT
210 220 230 240 250
huFGF-L AAGATTTCAAACAGAACCTCCCCAGCGCGCATGAAAGGACTTGATTAGCA
TTCTAAAGTTTGTCTTGGAGGGGTCGCGCGTACTTTCCTGAACTAATCGT
1. AB01265 110 120 130 140
[1790] CTTCTTTCACATGTCATTTGGC-CTCACTC-ACACCTGAGTCTGC-TG-C>
huFGF-L AAGATTTCAAACAGAACCTCCCCAGCGCGCATGAAAGGACTTGATTAGCA


260 270 280 290 300
huFGF-L TATGTCAAGAGGACCCGCTTATATACTCGGTGTGTATGTACACAGGACTC
ATACAGTTCTCCTGGGCGAATATATGAGCCACACATACATGTGTCCTGAG
1. AB01265 150 160 170 180 190
[1790] -TGCTGATGATGATGCCCCTCTC-TCAATGT-GGATTATGGTGATGACGG>
huFGF-L TATGTCAAGAGGACCCGCTTATATACTCGGTGTGTATGTACACAGGACTC
310 320 330 340 350
huFGF-L TGATCTGATCAGTTTGCGGAATTGGAGCCCCAGCCAACAGCCCTAGTCCT
ACTAGACTAGTCAAACGCCTTAACCTCGGGGTCGGTTGTCGGGATCAGGA
A T
1. AB01265 200 210 220 230 240
[1790] TG-ACTACGCTGCAT-GTGA-ATGGCCCTGCGATGAAAAGAAGCACTTTG>
huFGF-L TGATCTGATCAGTTTGCGGAATTGGAGCCCCAGCCAACAGCCCTAGTCCT
360 370 380 390 400
huFGF-L AGTATTGGCAGCGGCAGCTATAGATATTTCTGCAGAGCCAGCAGCCGGCT
TCATAACCGTCGCCGTCGATATCTATAAAGACGTCTCGGTCGTCGGCCGA
GTC
CTTT T
1. AB01265 250 260 270 280 290
[1790] CACATCCTTACCAGTGCCTTGCGAGGTGTGAACAGAGAGAGGAACTGTCG>
huFGF-L AGTATTGGCAGCGGCAGCTATAGATATTTCTGCAGAGCCAGCAGCCGGCT
410 420 430 440 450
huFGF-L CCCACCTACCCAAGGAGAGAAGATCGCTCCAAGACAGTGAGAGCTTCCCT
GGGTGGATGGGTTCCTCTCTTCTAGCGAGGTTCTGTCACTCTCGAAGGGA
1. AB01265 310 320 330 340
[1790] ACAACGTGCTTCATT-A-ACATA-T-G-TCAACTTGGCC-AATATACATA>
huFGF-L CCCACCTACCCAAGGAGAGAAGATCGCTCCAAGACAGTGAGAGCTTCCCT
460 470 480 490 500
huFGF-L GCCATTTCAGTGCAAAGTCCCTCCGGAGCGACCTCAGAGGAGTAACCGGG
CGGTAAAGTCACGTTTCAGGGAGGCCTCGCTGGAGTCTCCTCATTGGCCC
1. AB01265 350 360 370 380 390
[1790] GGCTTCGTACTTATAGCGGCCAGCAGCGCGCACTCA-GCTATTAGCCCAG>
huFGF-L GCCATTTCAGTGCAAAGTCCCTCCGGAGCGACCTCAGAGGAGTAACCGGG


510 520 530 540 550
huFGF-L CCTTAACTTTTTGCGCTCGTTTTGCTATAATTTTTCTCTATCCACCTCCA
GGAATTGAAAAACGCGAGCAAAACGATATTAAAAAGAGATAGGTGGAGGT
1. AB01265 400 410 420 430 440
[1790] AGCTCTGGAGAAGGTCACTACATGCCGAAACTGATC-TG-AC-CCGGAC->
huFGF-L CCTTAACTTTTTGCGCTCGTTTTGCTATAATTTTTCTCTATCCACCTCCA
560 570 580 590 600
huFGF-L TCCCACCCCCACAACACTCTTTACTGGGGGGGTCTTTTGTGTTCCGGATC
AGGGTGGGGGTGTTGTGAGAAATGACCCCCCCAGAAAACACAAGGCCTAG
GATC TCACCCG CA
1. AB01265 450 460 480 500
[1790] ACTTGTTTCACCAACGTTCTTTTTTGGTTTGGATTTGTGTGCCTTAGATA>
huFGF-L TCCCACCCCCACAACACTCTTTACTGGGGGGGTCTTTTGTGTTCCGGATC
610 620 630 640 650
huFGF-L TCCCCCTCCATGGCTCCCTTAGCCGAAGTCGGGGGCTTTCTGGGCGGCCT
AGGGGGAGGTACCGAGGGAATCGGCTTCAGCCCCCGAAAGACCCGCCGGA
1. AB01265 510 520 530 540 550
[1790] TTGCG-CACATGGCTCCTCTGGCCGACGTGGGCACCTTCCTCGGTGGGTA>
huFGF-L TCCCCCTCCATGGCTCCCTTAGCCGAAGTCGGGGGCTTTCTGGGCGGCCT
660 670 680 690 700
huFGF-L GGAGGGCTTGGGCCAGCAGGTGGGTTCGCATTTCCTGTTGCCTCCTGCCG
CCTCCCGAACCCGGTCGTCCACCCAAGCGTAAAGGACAACGGAGGACGGC
1. AB01265 560 570 580 590
[1790] TGATGCCCTTG---GGCAGGTGGGCTCCCACTTCTTGCTGCCGCCTGCCA>
huFGF-L GGAGGGCTTGGGCCAGCAGGTGGGTTCGCATTTCCTGTTGCCTCCTGCCG
710 720 730 740 750
huFGF-L GGGAGCGGCCGCCGCTGCTGGGCGAGCGCAGGAGCGCGGCGGAGCGGAGC
CCCTCGCCGGCGGCGACGACCCGCTCGCGTCCTCGCGCCGCCTCGCCTCG
C
1. AB01265 0 610 620 630 640
[1790] AGGACAGCCCCCTGCTCTTCAACG-ACCCACTGGCTAGTCGGAGCGACTT>
huFGF-L GGGAGCGGCCGCCGCTGCTGGGCGAGCGCAGGAGCGCGGCGGAGCGGAGC

```
                  760        770        780        790        800
huFGF-L      GCCCGCGGCGGGCCGGGGGCTGCGCAGCTGGCGCACCTGCACGGCATCCT
             CGGGCGCCGCCCGGCCCCCGACGCGTCGACCGCGTGGACGTGCCGTAGGA

1. AB01265   0          660            670        680        690
[ 1790 ]     TCCCGCAG--CGC---CCCCTCC-GACCTCTCCCATCTCCAGGGAATCTT>
              ||||| |   ||      || |  | ||  | || || || || ||| |
huFGF-L      GCCCGCGGCGGGCCGGGGGCTGCGCAGCTGGCGCACCTGCACGGCATCCT


                  810        820        830        840        850
huFGF-L      GCGCCGCCGGCAGCTCTATTGCCGCACCGGCTTCCACCTGCAGATCCTGC
             CGCGGCGGCCGTCGAGATAACGGCGTGGCCGAAGGTGGACGTCTAGGACG

1. AB01265       700        710        720        730        740
[ 1790 ]     GCGCCGCCGCCAGCTCTATTGTAGGACCGGCTTCCACCTGCAGATACTGC>
             ||||||||| ||||||||||  | ||||||||||||||||||| ||||
huFGF-L      GCGCCGCCGGCAGCTCTATTGCCGCACCGGCTTCCACCTGCAGATCCTGC


                  860        870        880        890        900
huFGF-L      CCGACGGCAGCGTGCAGGGCACCCGGCAGGACCACAGCCTCTTCGGTATC
             GGCTGCCGTCGCACGTCCCGTGGGCCGTCCTGGTGTCGGAGAAGCCATAG

1. AB01265       750        760        770        780        790
[ 1790 ]     CGGACGGGAACGTGCAGGGCACTCGGCAGGATCACAGCCGATTCGGTATC>
             | ||||| | |||||||||||| |||||||| |||||||  |||||||||
huFGF-L      CCGACGGCAGCGTGCAGGGCACCCGGCAGGACCACAGCCTCTTCGGTATC


                  910        920        930        940        950
huFGF-L      TTGGAATTCATCAGTGTGGCAGTGGGACTGGTCAGTATTAGAGGTGTGGA
             AACCTTAAGTAGTCACACCGTCACCCTGACCAGTCATAATCTCCACACCT

1. AB01265       800        810        820        830        840
[ 1790 ]     CTAGAATTTATCAGTGTTGCTATTGGCCTGGTTAGCATTCGAGGGGTCGA>
              | ||||| |||||||| ||  | || ||||| || ||| |||| || ||
huFGF-L      TTGGAATTCATCAGTGTGGCAGTGGGACTGGTCAGTATTAGAGGTGTGGA


                  960        970        980        990       1000
huFGF-L      CAGTGGTCTCTATCTTGGAATGAATGACAAAGGAGAACTCTATGGATCAG
             GTCACCAGAGATAGAACCTTACTTACTGTTTCCTCTTGAGATACCTAGTC

1. AB01265       850        860        870        880        890
[ 1790 ]     CACCGGCCTTTACCTTGGGATGAATGATAAAGGAGAACTTTTCGGATCGG>
             ||  || || || ||||| |||||||| |||||||||| |  ||||| |
huFGF-L      CAGTGGTCTCTATCTTGGAATGAATGACAAAGGAGAACTCTATGGATCAG
```


1010 1020 1030 1040 1050
huFGF-L AGAAACTTACTTCCGAATGCATCTTTAGGGAGCAGTTTGAAGAGAACTGG
TCTTTGAATGAAGGCTTACGTAGAAATCCCTCGTCAAACTTCTCTTGACC
1. AB01265 900 910 920 930 940
[1790] AAAAACTGACGTCCGAGTGCATTTTTCGGGAACAGTTTGAGGAGAACTGG>
huFGF-L AGAAACTTACTTCCGAATGCATCTTTAGGGAGCAGTTTGAAGAGAACTGG
1060 1070 1080 1090 1100
huFGF-L TATAACACCTATTCATCTAACATATATAAACATGGAGACACTGGCCGCAG
ATATTGTGGATAAGTAGATTGTATATATTTGTACCTCTGTGACCGGCGTC
1. AB01265 950 960 970 980 990
[1790] TACAACACCTATTCATCAAATCTATATAAACACGGAGACTCTGGACGGCG>
huFGF-L TATAACACCTATTCATCTAACATATATAAACATGGAGACACTGGCCGCAG
1110 1120 1130 1140 1150
huFGF-L GTATTTTGTGGCACTTAACAAAGACGGAACTCCAAGAGATGGCGCCAGGT
CATAAAACACCGTGAATTGTTTCTGCCTTGAGGTTCTCTACCGCGGTCCA
1. AB01265 1000 1010 1020 1030 1040
[1790] ATACTTTGTAGCACTTAACAAAGATGGGACCCCTAGAGATGGCACCAGAG>
huFGF-L GTATTTTGTGGCACTTAACAAAGACGGAACTCCAAGAGATGGCGCCAGGT
1160 1170 1180 1190 1200
huFGF-L CCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATCCA
GGTTCTCCGTAGTCTTTAAATGTGTAAAGAATGGATCTGGTCACCTAGGT
1. AB01265 1050 1060 1070 1080 1090
[1790] CTAAGAGACATCAGAAGTTCACACATTTTTTGCCCAGACCTGTCGATCCT>
huFGF-L CCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATCCA
1210 1220 1230 1240 1250
huFGF-L GAAAGAGTTCCAGAATTGTACAAGGACCTACTGATGTACACTTGAAGTGC
CTTTCTCAAGGTCTTAACATGTTCCTGGATGACTACATGTGAACTTCACG
1. AB01265 1100 1110 1120 1130 1140
[1790] GAAAAAGTTCCTGAACTCTATAAAGATCTCATGGGATACAGCTGAA-GCA>
huFGF-L GAAAGAGTTCCAGAATTGTACAAGGACCTACTGATGTACACTTGAAGTGC

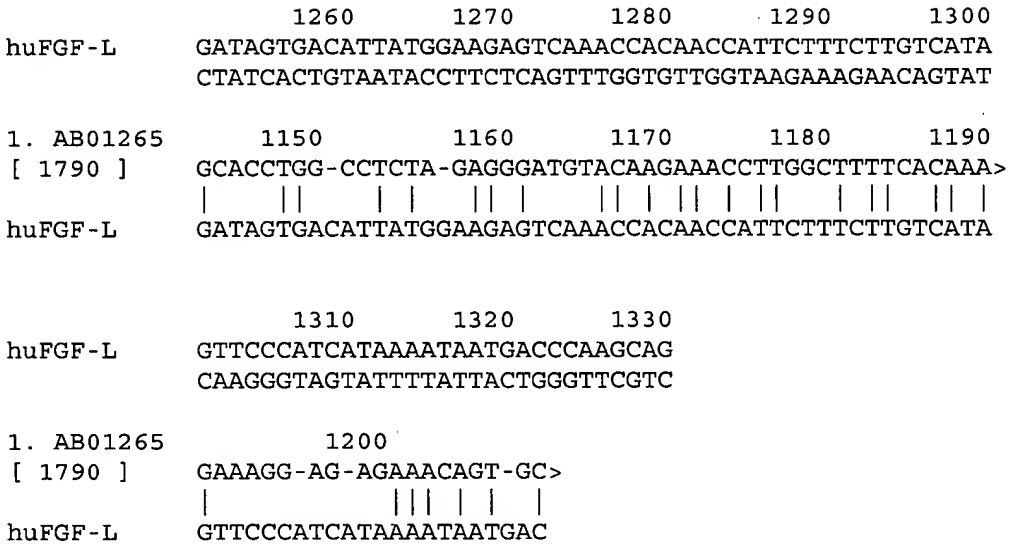
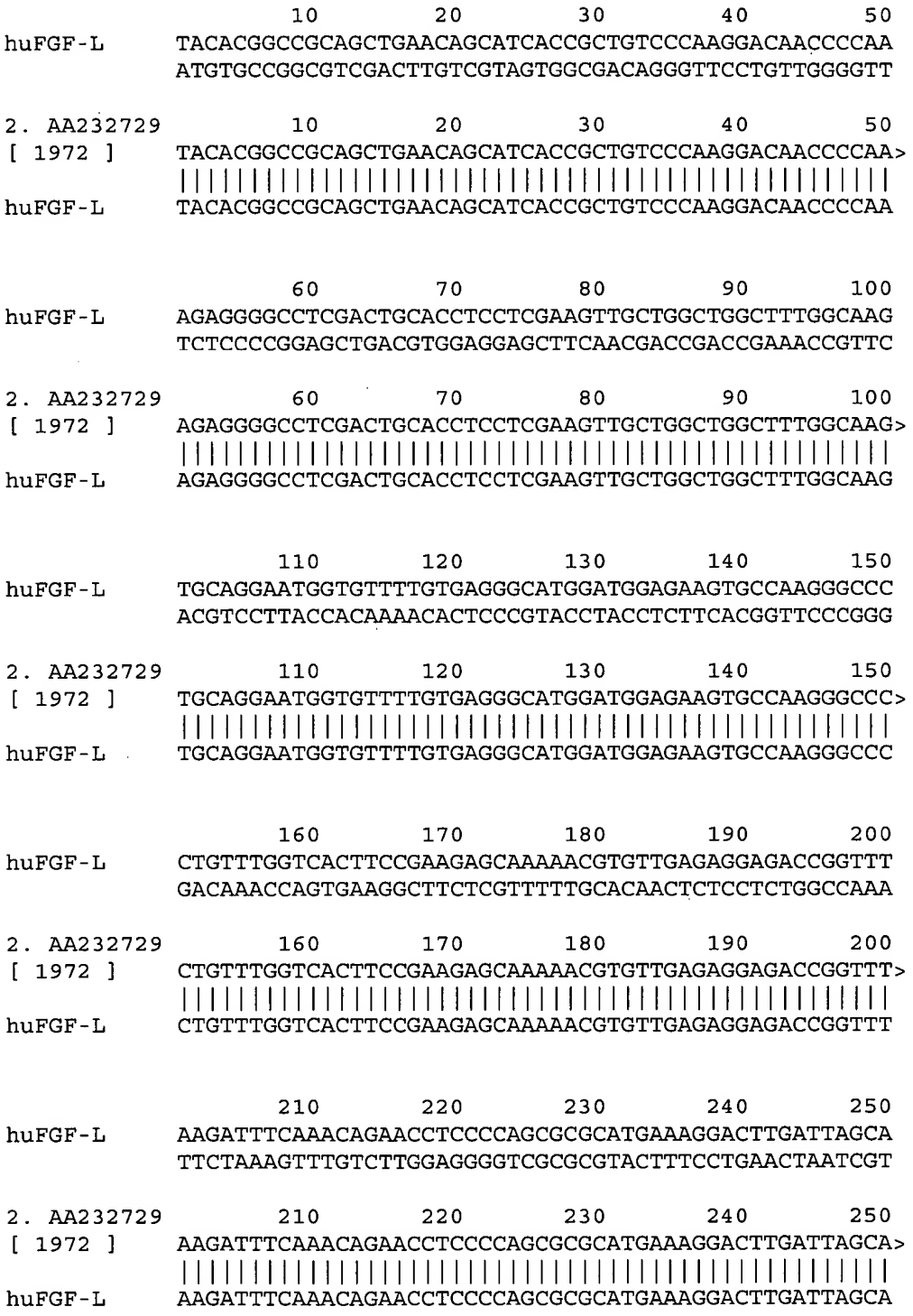

1260 1270 1280 1290 1300
huFGF-L GATAGTGACATTATGGAAGAGTCAAACCACAACCATTCTTTCTTGTCATA
CTATCACTGTAATACCTTCTCAGTTTGGTGTTGGTAAGAAAGAACAGTAT
1. AB01265 1150 1160 1170 1180 1190
[1790] GCACCTGG-CCTCTA-GAGGGATGTACAAGAAACCTTGGCTTTTCACAAA>
huFGF-L GATAGTGACATTATGGAAGAGTCAAACCACAACCATTCTTTCTTGTCATA
1310 1320 1330
huFGF-L GTTCCCATCATAAAATAATGACCCAAGCAG
CAAGGGTAGTATTTTATTACTGGGTTCGTC
1. AB01265 1200
[1790] GAAAGG-AG-AGAAACAGT-GC>
huFGF-L GTTCCCATCATAAAATAATGAC

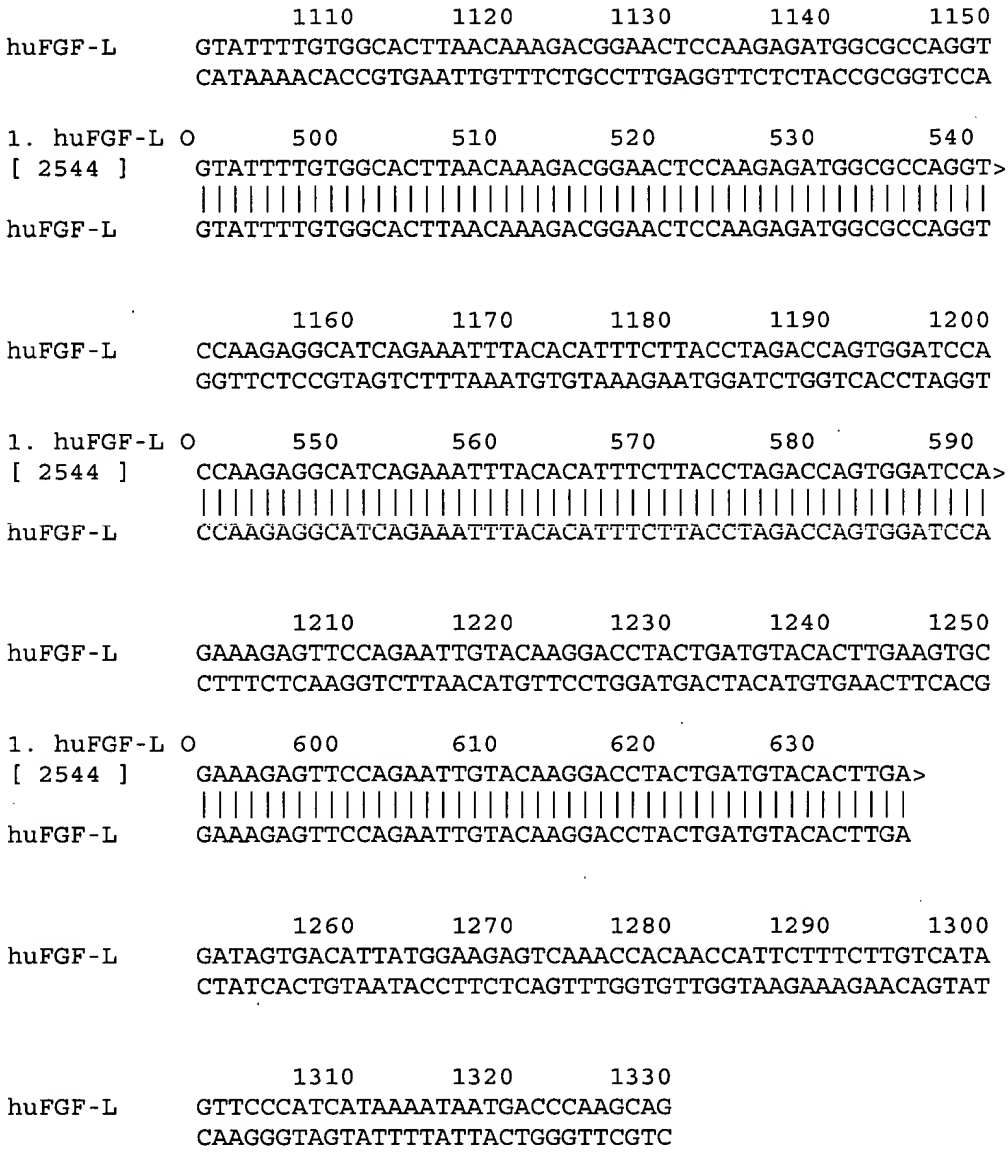
EXHIBIT G


10 20 30 40 50
huFGF-L TACACGGCCGCAGCTGAACAGCATCACCGCTGTCCCAAGGACAACCCCAA
ATGTGCCGGCGTCGACTTGTCGTAGTGGCGACAGGGTTCCTGTTGGGGTT
2. AA232729 10 20 30 40 50
[1972] TACACGGCCGCAGCTGAACAGCATCACCGCTGTCCCAAGGACAACCCCAA>
huFGF-L TACACGGCCGCAGCTGAACAGCATCACCGCTGTCCCAAGGACAACCCCAA
60 70 80 90 100
huFGF-L AGAGGGGCCTCGACTGCACCTCCTCGAAGTTGCTGGCTGGCTTTGGCAAG
TCTCCCCGGAGCTGACGTGGAGGAGCTTCAACGACCGACCGAAACCGTTC
2. AA232729 60 70 80 90 100
[1972] AGAGGGGCCTCGACTGCACCTCCTCGAAGTTGCTGGCTGGCTTTGGCAAG>
huFGF-L AGAGGGGCCTCGACTGCACCTCCTCGAAGTTGCTGGCTGGCTTTGGCAAG
110 120 130 140 150
huFGF-L TGCAGGAATGGTGTTTTGTGAGGGCATGGATGGAGAAGTGCCAAGGGCCC
ACGTCCTTACCACAAAACACTCCCGTACCTACCTCTTCACGGTTCCCGGG
2. AA232729 110 120 130 140 150
[1972] TGCAGGAATGGTGTTTTGTGAGGGCATGGATGGAGAAGTGCCAAGGGCCC>
huFGF-L TGCAGGAATGGTGTTTTGTGAGGGCATGGATGGAGAAGTGCCAAGGGCCC
160 170 180 190 200
huFGF-L CTGTTTGGTCACTTCCGAAGAGCAAAAACGTGTTGAGAGGAGACCGGTTT
GACAAACCAGTGAAGGCTTCTCGTTTTTGCACAACTCTCCTCTGGCCAAA
2. AA232729 160 170 180 190 200
[1972] CTGTTTGGTCACTTCCGAAGAGCAAAAACGTGTTGAGAGGAGACCGGTTT>
huFGF-L CTGTTTGGTCACTTCCGAAGAGCAAAAACGTGTTGAGAGGAGACCGGTTT
210 220 230 240 250
huFGF-L AAGATTTCAAACAGAACCTCCCCAGCGCGCATGAAAGGACTTGATTAGCA
TTCTAAAGTTTGTCTTGGAGGGGTCGCGCGTACTTTCCTGAACTAATCGT
2. AA232729 210 220 230 240 250
[1972] AAGATTTCAAACAGAACCTCCCCAGCGCGCATGAAAGGACTTGATTAGCA>
huFGF-L AAGATTTCAAACAGAACCTCCCCAGCGCGCATGAAAGGACTTGATTAGCA

```
                    260        270        280        290        300
huFGF-L     TATGTCAAGAGGACCCGCTTATATACTCGGTGTGTATGTACACAGGACTC
            ATACAGTTCTCCTGGGCGAATATATGAGCCACACATACATGTGTCCTGAG

2. AA232729         260        270        280        290        300
[ 1972 ]    TATGTCAAGAGGACCCGCTTATATACTCGGTGTGTATGTACACAGGACTC>
            ||||||||||||||||||||||||||||||||||||||||||||||||||
huFGF-L     TATGTCAAGAGGACCCGCTTATATACTCGGTGTGTATGTACACAGGACTC


                    310        320        330        340        350
huFGF-L     TGATCTGATCAGTTTGCGGAATTGGAGCCCCAGCCAACAGCCCTAGTCCT
            ACTAGACTAGTCAAACGCCTTAACCTCGGGGTCGGTTGTCGGGATCAGGA

2. AA232729         310        320        330        340        350
[ 1972 ]    TGATCTGATCAGTTTGCGGAATTGGAGCCCCAGCCAACAGCCCTAGTCCT>
            ||||||||||||||||||||||||||||||||||||||||||||||||||
huFGF-L     TGATCTGATCAGTTTGCGGAATTGGAGCCCCAGCCAACAGCCCTAGTCCT


                    360        370        380        390        400
huFGF-L     AGTATTGGCAGCGGCAGCTATAGATATTTCTGCAGAGCCAGCAGCCGGCT
            TCATAACCGTCGCCGTCGATATCTATAAAGACGTCTCGGTCGTCGGCCGA

2. AA232729         360        370        380        390        400
[ 1972 ]    AGTATTGGCAGCGGCACGTATAGATATTTCTGCAGAGCCAGCAGCCGGCT>
            |||||||||||||||| ||||||||||||||||||||||||||||||||
huFGF-L     AGTATTGGCAGCGGCAGCTATAGATATTTCTGCAGAGCCAGCAGCCGGCT


                    410        420        430        440        450
huFGF-L     CCCACCTACCCAAGGAGAGAAGATCGCTCCAAGACAGTGAGAGCTTCCCT
            GGGTGGATGGGTTCCTCTCTTCTAGCGAGGTTCTGTCACTCTCGAAGGGA

2. AA232729         410        420        430        440        450
[ 1972 ]    CCCACCTACCCAAGGAGAGAAGATCGCTCCAAGACAGTGAGAGCTTCCCT>
            ||||||||||||||||||||||||||||||||||||||||||||||||||
huFGF-L     CCCACCTACCCAAGGAGAGAAGATCGCTCCAAGACAGTGAGAGCTTCCCT


                    460        470        480        490        500
huFGF-L     GCCATTTCAGTGCAAAGTCCCTCCGGAGCGACCTCAGAGGAGTAACCGGG
            CGGTAAAGTCACGTTTCAGGGAGGCCTCGCTGGAGTCTCCTCATTGGCCC

2. AA232729         460        470        480        490
[ 1972 ]    GCCATTTCAGTGCAAAGTCCCTCCGGAGCGACCTCAGAGGAGTAAC>
            ||||||||||||||||||||||||||||||||||||||||||||||||
huFGF-L     GCCATTTCAGTGCAAAGTCCCTCCGGAGCGACCTCAGAGGAGTAAC


                    510        520        530        540        550
huFGF-L     CCTTAACTTTTTGCGCTCGTTTTGCTATAATTTTTCTCTATCCACCTCCA
            GGAATTGAAAAACGCGAGCAAAACGATATTAAAAAGAGATAGGTGGAGGT
```

```
                  560        570        580        590        600
huFGF-L      TCCCACCCCCACAACACTCTTTACTGGGGGGGTCTTTTGTGTTCCGGATC
             AGGGTGGGGGTGTTGTGAGAAATGACCCCCCCAGAAAACACAAGGCCTAG

                  610        620        630        640        650
huFGF-L      TCCCCCTCCATGGCTCCCTTAGCCGAAGTCGGGGGCTTTCTGGGCGGCCT
             AGGGGGAGGTACCGAGGGAATCGGCTTCAGCCCCCGAAAGACCCGCCGGA

1. huFGF-L O                  10         20         30         40
[ 2544 ]                ATGGCTCCCTTAGCCGAAGTCGGGGGCTTTCTGGGCGGCCT>
                        ||||||||||||||||||||||||||||||||||||||||
huFGF-L                 ATGGCTCCCTTAGCCGAAGTCGGGGGCTTTCTGGGCGGCCT

                  660        670        680        690        700
huFGF-L      GGAGGGCTTGGGCCAGCAGGTGGGTTCGCATTTCCTGTTGCCTCCTGCCG
             CCTCCCGAACCCGGTCGTCCACCCAAGCGTAAAGGACAACGGAGGACGGC

1. huFGF-L O       50         60         70         80         90
[ 2544 ]     GGAGGGCTTGGGCCAGCAGGTGGGTTCGCATTTCCTGTTGCCTCCTGCCG>
             ||||||||||||||||||||||||||||||||||||||||||||||||||
huFGF-L      GGAGGGCTTGGGCCAGCAGGTGGGTTCGCATTTCCTGTTGCCTCCTGCCG

                  710        720        730        740        750
huFGF-L      GGGAGCGGCCGCCGCTGCTGGGCGAGCGCAGGAGCGCGGCGGAGCGGAGC
             CCCTCGCCGGCGGCGACGACCCGCTCGCGTCCTCGCGCCGCCTCGCCTCG

1. huFGF-L O      100        110        120        130        140
[ 2544 ]     GGGAGCGGCCGCCGCTGCTGGGCGAGCGCAGGAGCGCGGCGGAGCGGAGC>
             ||||||||||||||||||||||||||||||||||||||||||||||||||
huFGF-L      GGGAGCGGCCGCCGCTGCTGGGCGAGCGCAGGAGCGCGGCGGAGCGGAGC

                  760        770        780        790        800
huFGF-L      GCCCGCGGCGGGCCGGGGGCTGCGCAGCTGGCGCACCTGCACGGCATCCT
             CGGGCGCCGCCCGGCCCCCGACGCGTCGACCGCGTGGACGTGCCGTAGGA

1. huFGF-L O      150        160        170        180        190
[ 2544 ]     GCCCGCGGCGGGCCGGGGGCTGCGCAGCTGGCGCACCTGCACGGCATCCT>
             ||||||||||||||||||||||||||||||||||||||||||||||||||
huFGF-L      GCCCGCGGCGGGCCGGGGGCTGCGCAGCTGGCGCACCTGCACGGCATCCT

                  810        820        830        840        850
huFGF-L      GCGCCGCCGGCAGCTCTATTGCCGCACCGGCTTCCACCTGCAGATCCTGC
             CGCGGCGGCCGTCGAGATAACGGCGTGGCCGAAGGTGGACGTCTAGGACG

1. huFGF-L O      200        210        220        230        240
[ 2544 ]     GCGCCGCCGGCAGCTCTATTGCCGCACCGGCTTCCACCTGCAGATCCTGC>
             ||||||||||||||||||||||||||||||||||||||||||||||||||
huFGF-L      GCGCCGCCGGCAGCTCTATTGCCGCACCGGCTTCCACCTGCAGATCCTGC
```

```
                  860        870        880        890        900
huFGF-L      CCGACGGCAGCGTGCAGGGCACCCGGCAGGACCACAGCCTCTTCGGTATC
             GGCTGCCGTCGCACGTCCCGTGGGCCGTCCTGGTGTCGGAGAAGCCATAG

1. huFGF-L O       250        260        270        280        290
[ 2544 ]     CCGACGGCAGCGTGCAGGGCACCCGGCAGGACCACAGCCTCTTCGGTATC>
             ||||||||||||||||||||||||||||||||||||||||||||||||||
huFGF-L      CCGACGGCAGCGTGCAGGGCACCCGGCAGGACCACAGCCTCTTCGGTATC


                  910        920        930        940        950
huFGF-L      TTGGAATTCATCAGTGTGGCAGTGGGACTGGTCAGTATTAGAGGTGTGGA
             AACCTTAAGTAGTCACACCGTCACCCTGACCAGTCATAATCTCCACACCT

1. huFGF-L O       300        310        320        330        340
[ 2544 ]     TTGGAATTCATCAGTGTGGCAGTGGGACTGGTCAGTATTAGAGGTGTGGA>
             ||||||||||||||||||||||||||||||||||||||||||||||||||
huFGF-L      TTGGAATTCATCAGTGTGGCAGTGGGACTGGTCAGTATTAGAGGTGTGGA


                  960        970        980        990       1000
huFGF-L      CAGTGGTCTCTATCTTGGAATGAATGACAAAGGAGAACTCTATGGATCAG
             GTCACCAGAGATAGAACCTTACTTACTGTTTCCTCTTGAGATACCTAGTC

1. huFGF-L O       350        360        370        380        390
[ 2544 ]     CAGTGGTCTCTATCTTGGAATGAATGACAAAGGAGAACTCTATGGATCAG>
             ||||||||||||||||||||||||||||||||||||||||||||||||||
huFGF-L      CAGTGGTCTCTATCTTGGAATGAATGACAAAGGAGAACTCTATGGATCAG


                 1010       1020       1030       1040       1050
huFGF-L      AGAAACTTACTTCCGAATGCATCTTTAGGGAGCAGTTTGAAGAGAACTGG
             TCTTTGAATGAAGGCTTACGTAGAAATCCCTCGTCAAACTTCTCTTGACC

1. huFGF-L O       400        410        420        430        440
[ 2544 ]     AGAAACTTACTTCCGAATGCATCTTTAGGGAGCAGTTTGAAGAGAACTGG>
             ||||||||||||||||||||||||||||||||||||||||||||||||||
huFGF-L      AGAAACTTACTTCCGAATGCATCTTTAGGGAGCAGTTTGAAGAGAACTGG


                 1060       1070       1080       1090       1100
huFGF-L      TATAACACCTATTCATCTAACATATATAAACATGGAGACACTGGCCGCAG
             ATATTGTGGATAAGTAGATTGTATATATTTGTACCTCTGTGACCGGCGTC

1. huFGF-L O       450        460        470        480        490
[ 2544 ]     TATAACACCTATTCATCTAACATATATAAACATGGAGACACTGGCCGCAG>
             ||||||||||||||||||||||||||||||||||||||||||||||||||
huFGF-L      TATAACACCTATTCATCTAACATATATAAACATGGAGACACTGGCCGCAG
```


1110 1120 1130 1140 1150
huFGF-L GTATTTTGTGGCACTTAACAAAGACGGAACTCCAAGAGATGGCGCCAGGT
CATAAAACACCGTGAATTGTTTCTGCCTTGAGGTTCTCTACCGCGGTCCA
1. huFGF-L O 500 510 520 530 540
[2544] GTATTTTGTGGCACTTAACAAAGACGGAACTCCAAGAGATGGCGCCAGGT>
huFGF-L GTATTTTGTGGCACTTAACAAAGACGGAACTCCAAGAGATGGCGCCAGGT
1160 1170 1180 1190 1200
huFGF-L CCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATCCA
GGTTCTCCGTAGTCTTTAAATGTGTAAAGAATGGATCTGGTCACCTAGGT
1. huFGF-L O 550 560 570 580 590
[2544] CCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATCCA>
huFGF-L CCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATCCA
1210 1220 1230 1240 1250
huFGF-L GAAAGAGTTCCAGAATTGTACAAGGACCTACTGATGTACACTTGAAGTGC
CTTTCTCAAGGTCTTAACATGTTCCTGGATGACTACATGTGAACTTCACG
1. huFGF-L O 600 610 620 630
[2544] GAAAGAGTTCCAGAATTGTACAAGGACCTACTGATGTACACTTGA>
huFGF-L GAAAGAGTTCCAGAATTGTACAAGGACCTACTGATGTACACTTGA
1260 1270 1280 1290 1300
huFGF-L GATAGTGACATTATGGAAGAGTCAAACCACAACCATTCTTTCTTGTCATA
CTATCACTGTAATACCTTCTCAGTTTGGTGTTGGTAAGAAAGAACAGTAT
1310 1320 1330
huFGF-L GTTCCCATCATAAAATAATGACCCAAGCAG
CAAGGGTAGTATTTTATTACTGGGTTCGTC